

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 15:41:08 ; Search time 33.4091 Seconds

(without alignments)  
277.441 Million cell updates/sec

Title: US-09-744-875A-1

Perfect score: 21

Sequence: 1 agatttcaggaatccaatc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 830498

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	18	85.7	21	1	US-08-366-276-8	Sequence 8, Appli
2	18	85.7	100	4	US-09-522-217-59	Sequence 59, Appli
3	18	85.7	100	4	US-09-522-217-60	Sequence 60, Appli
4	15.4	73.3	24	4	US-08-369-754-1	Sequence 1, Appli
5	14.6	69.5	58	3	US-09-140-804-46	Sequence 46, Appli
6	14.6	69.5	58	4	US-09-173-043-22	Sequence 22, Appli
7	14.6	69.5	58	4	US-09-209-525-42	Sequence 42, Appli
8	14.6	69.5	58	4	US-09-686-838B-46	Sequence 46, Appli
9	14.2	67.6	20	4	US-09-662-402A-35	Sequence 35, Appli
10	13.8	65.7	30	1	US-08-201-697-12	Sequence 12, Appli
11	13.8	65.7	30	1	US-08-463-090B-24	Sequence 24, Appli
12	13.6	64.8	34	1	US-08-332-420-54	Sequence 54, Appli
13	13.6	64.8	37	1	US-07-941-363-1	Sequence 1, Appli
14	13.6	64.8	38	1	US-09-143-634-28	Sequence 28, Appli
15	13.6	64.8	40	1	US-08-308-196A-4	Sequence 4, Appli
16	13.6	64.8	40	3	US-09-289-803-3	Sequence 3, Appli
17	13.6	64.8	40	5	PCT-US91-06452-4	Sequence 4, Appli
18	13.6	64.8	41	3	US-09-289-803-2	Sequence 2, Appli
19	13.6	64.8	42	3	US-09-289-803-1	Sequence 1, Appli
20	13.6	64.8	68	6	5221737-7	Patent No. 5221737
21	13.4	63.8	30	3	US-09-030-613-30	Sequence 30, Appli
22	13.4	63.8	30	4	US-09-451-905-30	Sequence 30, Appli
23	13.4	63.8	40	4	US-09-313-221A-17	Sequence 77, Appli
24	13.2	62.9	25	3	US-08-840-316-5	Sequence 5, Appli
25	13.2	62.9	25	3	US-08-809-523-5	Sequence 5, Appli
26	13.2	62.9	25	3	US-08-471-971-5	Sequence 5, Appli
27	13.2	62.9	25	4	US-09-402-776-5	Sequence 5, Appli

C 28	13.2	62.9	25	5	PCT-US93-08849A-5	Sequence 5, Appli
C 29	13.2	62.9	25	5	PCT-US93-08849-5	Sequence 5, Appli
C 30	13.2	62.9	31	3	US-09-182-816-30	Sequence 30, Appli
C 31	13.2	62.9	31	3	US-09-471-528-30	Sequence 30, Appli
C 32	13.2	62.9	31	3	US-09-634-530-30	Sequence 30, Appli
C 33	13.2	62.9	33	1	US-07-955-041-6	Sequence 6, Appli
C 34	13.2	62.9	33	1	US-08-227-455-6	Sequence 6, Appli
C 35	13.2	62.9	33	1	US-08-472-482-6	Sequence 6, Appli
C 36	13.2	62.9	33	1	US-08-487-063-6	Sequence 6, Appli
C 37	13.2	62.9	33	4	US-08-169-715-47	Sequence 47, Appli
C 38	13.2	62.9	63	3	US-09-140-804-38	Sequence 38, Appli
C 39	13.2	62.9	63	4	US-09-686-838B-38	Sequence 38, Appli
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C 43	13.2	62.9	21	2	US-08-653-382A-14	Sequence 14, Appli
C 44	13.2	62.9	26	2	US-08-215-089-4	Sequence 4, Appli
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C 46	13.2	62.9	27	1	US-08-480-604A-15	Sequence 15, Appli
C 47	13.2	62.9	27	2	US-08-405-496A-15	Sequence 15, Appli
C 48	13.2	62.9	27	3	US-08-915-136-15	Sequence 15, Appli
C 49	13.2	62.9	27	4	US-08-957-310-15	Sequence 15, Appli
C 50	13.2	62.9	27	4	US-10-011-366-15	Sequence 15, Appli
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C 53	13.2	62.9	35	5	PCT-US95-09458-2	Sequence 2, Appli
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C 59	13.2	62.9	62	1	US-07-907-710A-16	Sequence 16, Appli
C 60	13.2	62.9	62	1	US-08-209-182C-16	Sequence 16, Appli
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C 63	13.2	62.9	70	3	US-09-225-510-8	Sequence 8, Appli
C 64	13.2	62.9	96	5	PCT-US94-06466-23	Sequence 23, Appli
C 65	13.2	62.9	96	5	PCT-US94-06466-52	Sequence 52, Appli
C 66	12.8	61.0	21	1	US-08-044-621D-11	Sequence 11, Appli
C 67	12.8	61.0	30	1	US-08-722-001-9	Sequence 9, Appli
C 68	12.8	61.0	32	4	US-09-485-737B-54	Sequence 54, Appli
C 69	12.8	61.0	43	1	US-08-741-881-38	Sequence 38, Appli
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C 72	12.8	61.0	43	3	US-08-404-796-38	Sequence 38, Appli
C 73	12.8	61.0	43	3	US-08-931-869-38	Sequence 38, Appli
C 74	12.8	61.0	43	4	US-09-350-399-38	Sequence 38, Appli
C 75	12.8	61.0	43	4	US-09-236-140A-38	Sequence 38, Appli
C 76	12.8	61.0	43	4	US-09-415-784-38	Sequence 38, Appli
C 77	12.8	61.0	43	4	US-09-415-785A-38	Sequence 38, Appli
C 78	12.8	61.0	43	4	US-08-944-465-38	Sequence 38, Appli
C 79	12.8	61.0	43	4	US-09-415-900-38	Sequence 38, Appli
C 80	12.8	61.0	43	4	US-09-415-900-38	Sequence 38, Appli
C 81	12.8	61.0	61	3	US-09-275-850-80	Sequence 80, Appli
C 82	12.8	61.0	61	3	US-09-275-850-80	Sequence 80, Appli
C 83	12.8	61.0	61	3	US-09-275-850-80	Sequence 80, Appli
C 84	12.6	60.0	21	3	US-09-003-903-2	Sequence 2, Appli
C 85	12.6	60.0	27	1	US-08-647-928-1	Sequence 1, Appli
C 86	12.6	60.0	27	4	US-09-662-402A-38	Sequence 38, Appli
C 87	12.6	60.0	30	2	US-08-647-977-9	Sequence 9, Appli
C 88	12.6	60.0	48	1	US-08-477-254A-33	Sequence 33, Appli
C 89	12.6	60.0	48	2	US-08-477-254B-33	Sequence 33, Appli
C 90	12.6	60.0	48	2	US-08-428-734B-33	Sequence 33, Appli
C 91	12.6	60.0	48	2	US-08-713-556B-33	Sequence 33, Appli
C 92	12.6	60.0	80	4	US-09-157-748-43	Sequence 43, Appli
C 93	12.4	59.0	20	2	US-08-299-074A-25	Sequence 25, Appli
C 94	12.4	59.0	20	2	US-08-329-074A-25	Sequence 25, Appli
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C 96	12.4	59.0	20	4	US-09-517-467B-56	Sequence 25, Appli
C 97	12.4	59.0	21	4	US-09-422-978-10711	Sequence 10711, A
C 98	12.4	59.0	30	2	US-08-577-492-26	Sequence 26, Appli
C 99	12.4	59.0	30	2	US-08-969-714-8	Sequence 8, Appli
C 100	12.4	59.0	30	3	US-09-079-630-26	Sequence 26, Appli

101	12.4	59.0	36	4	US-09-622-540A-4	Sequence 4, Appli	174	12	57.1	30	4	US-09-477-763-6	Sequence 6, Appli
102	12.4	59.0	36	4	US-09-622-540A-4	Sequence 4, Appli	175	12	57.1	30	4	US-09-590-774-6	Sequence 6, Appli
103	12.4	59.0	40	2	US-08-343-443B-32	Sequence 32, Appli	176	12	57.1	30	4	US-09-480-993-5	Sequence 5, Appli
104	12.4	59.0	40	4	US-09-332-902-5	Sequence 5, Appli	177	12	57.1	30	4	US-09-367-065A-5	Sequence 5, Appli
105	12.4	59.0	40	4	US-09-332-902-7	Sequence 7, Appli	178	12	57.1	30	4	US-09-619-550-6	Sequence 6, Appli
106	12.4	59.0	47	4	US-09-422-978-322	Sequence 322, App	179	12	57.1	30	4	US-09-240-734-6	Sequence 6, Appli
107	12.2	58.1	21	1	US-08-266-080B-7	Sequence 7, Appli	180	12	57.1	30	4	US-09-231-253-6	Sequence 6, Appli
108	12.2	58.1	21	4	US-09-422-978-8328	Sequence 8328, Ap	181	12	57.1	30	4	US-09-724-958-6	Sequence 6, Appli
109	12.2	58.1	21	5	PCT-US95-05423-7	Sequence 7, Appli	182	12	57.1	30	4	US-09-481-620A-29	Sequence 29, Appli
110	12.2	58.1	24	1	US-08-125-012-28	Sequence 28, Appli	183	12	57.1	30	4	US-09-696-322-6	Sequence 6, Appli
111	12.2	58.1	24	1	US-08-221-579A-22	Sequence 22, Appli	184	12	57.1	30	4	US-09-717-391-6	Sequence 6, Appli
112	12.2	58.1	24	1	US-08-783-818-28	Sequence 28, Appli	185	12	57.1	30	4	US-09-686-466-5	Sequence 5, Appli
113	12.2	58.1	24	2	US-08-453-349-28	Sequence 28, Appli	186	12	57.1	30	4	US-09-568-466-5	Sequence 5, Appli
114	12.2	58.1	24	2	US-08-710-30A-9	Sequence 9, Appli	187	12	57.1	31	4	US-09-240-307-6	Sequence 6, Appli
115	12.2	58.1	24	2	US-08-979-385B-26	Sequence 26, Appli	188	12	57.1	31	4	US-09-556-877-216	Sequence 216, App
116	12.2	58.1	24	2	US-08-338-579A-59	Sequence 59, Appli	189	12	57.1	31	4	US-09-620-412C-216	Sequence 216, App
117	12.2	58.1	24	3	US-09-321-461-22	Sequence 22, Appli	190	12	57.1	31	4	US-09-598-419-216	Sequence 6, Appli
118	12.2	58.1	24	3	US-09-321-461-22	Sequence 22, Appli	191	12	57.1	32	2	US-08-577-492-6	Sequence 6, Appli
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120	12.2	58.1	24	4	US-08-880-576-28	Sequence 28, Appli	193	12	57.1	32	3	US-09-623-062-15	Sequence 15, Appli
121	12.2	58.1	24	4	US-09-996-243-190	Sequence 190, App	194	12	57.1	33	3	US-08-827-171B-10	Sequence 108, App
122	12.2	58.1	24	5	PCT-US94-09851-59	Sequence 59, Appli	195	12	57.1	35	3	US-09-143-634-19	Sequence 19, Appli
123	12.2	58.1	24	5	PCT-US95-16206A-14	Sequence 14, Appli	196	12	57.1	36	4	US-09-000-094-18	Sequence 18, Appli
124	12.2	58.1	26	3	US-09-374-135-17	Sequence 17, Appli	197	12	57.1	36	4	US-09-269-262B-14	Sequence 9, Appli
125	12.2	58.1	30	3	US-09-275-850-166	Sequence 166, App	198	12	57.1	37	4	US-09-043-816E-9	Sequence 7, Appli
126	12.2	58.1	30	3	US-09-019-793A-99	Sequence 99, Appli	199	12	57.1	37	4	US-09-731-030A-7	Sequence 3, Appli
127	12.2	58.1	31	3	US-08-836-402B-5	Sequence 5, Appli	200	12	57.1	38	1	US-07-988-194A-3	Sequence 11, Appli
128	12.2	58.1	33	3	US-08-108-020-25	Sequence 25, Appli	201	12	57.1	38	1	US-08-258-152-11	Sequence 11, Appli
129	12.2	58.1	38	3	US-08-945-726-2	Sequence 2, Appli	202	12	57.1	38	2	US-08-076-299A-11	Sequence 11, Appli
130	12.2	58.1	46	1	US-08-136-119-18	Sequence 18, Appli	203	12	57.1	38	2	US-08-438-882-11	Sequence 237, App
131	12.2	58.1	46	4	US-09-091-042A-3	Sequence 3, Appli	204	12	57.1	38	3	US-08-444-818-237	Sequence 11, Appli
132	12.2	58.1	53	3	US-08-388-029A-50	Sequence 50, Appli	205	12	57.1	38	4	US-09-266-596-11	Sequence 3, Appli
133	12.2	58.1	53	3	US-08-388-029A-50	Sequence 50, Appli	206	12	57.1	38	4	US-08-475-442A-3	Sequence 11, Appli
134	12.2	58.1	58	3	US-09-275-850-235	Sequence 235, App	207	12	57.1	38	4	US-09-944-411-11	Sequence 4, Appli
135	12.2	58.1	58	3	US-09-275-850-238	Sequence 238, App	208	12	57.1	43	5	PCT-US92-0101E-4	Sequence 94, Appli
136	12.2	58.1	60	1	US-08-143-219-18	Sequence 18, Appli	209	12	57.1	50	3	US-09-091-814-94	Sequence 4, Appli
137	12.2	58.1	61	3	US-08-870-930-45	Sequence 45, Appli	210	12	57.1	51	1	US-08-319-621A-9	Sequence 48, Appli
138	12.2	58.1	61	4	US-09-254-968-48	Sequence 48, Appli	211	12	57.1	51	1	US-08-388-029A-48	Sequence 55, Appli
139	12.2	58.1	64	4	US-09-653-403-9	Sequence 9, Appli	212	12	57.1	60	3	US-08-643-704A-3	Sequence 3, Appli
140	12.2	58.1	64	4	US-10-013-784-9	Sequence 9, Appli	213	12	57.1	60	3	US-08-643-704A-22	Sequence 22, Appli
141	12.2	58.1	67	4	US-09-519-729-3	Sequence 3, Appli	214	12	57.1	53	3	US-08-388-029A-55	Sequence 55, Appli
142	12.2	58.1	89	3	US-09-488-295-9	Sequence 9, Appli	215	12	57.1	53	3	US-08-643-704A-3	Sequence 3, Appli
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144	12.2	58.1	100	1	US-08-145-705A-28	Sequence 28, Appli	217	12	57.1	97	1	US-08-210-222-17	Sequence 17, Appli
145	12.2	57.1	12	3	US-09-593-323-39	Sequence 39, Appli	218	12	57.1	97	4	US-09-415-216C-1	Sequence 25, Appli
146	12.2	57.1	12	3	US-09-594-108-39	Sequence 39, Appli	219	12	57.1	98	5	PCT-US94-06456-25	Sequence 54, Appli
147	12.2	57.1	12	3	US-09-344-300-39	Sequence 39, Appli	220	12	57.1	98	5	PCT-US94-06456-25	Sequence 2074, Ap
148	12.2	57.1	20	3	US-09-021-701-596	Sequence 13, Appli	221	11.8	56.2	15	2	US-08-585-684B-2074	Sequence 27, Appli
149	12.2	57.1	24	3	US-08-948-378A-13	Sequence 13, Appli	222	11.8	56.2	21	1	US-08-477-254A-27	Sequence 27, Appli
150	12.2	57.1	24	3	US-08-948-378A-13	Sequence 13, Appli	223	11.8	56.2	21	2	US-08-477-254A-27	Sequence 27, Appli
151	12.2	57.1	24	3	US-09-169-425C-13	Sequence 13, Appli	224	11.8	56.2	21	2	US-08-428-734B-27	Sequence 27, Appli
152	12.2	57.1	24	3	US-09-169-425C-15	Sequence 15, Appli	225	11.8	56.2	21	2	US-08-713-556F-27	Sequence 6, Appli
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154	12.2	57.1	26	3	US-08-746-559A-6	Sequence 6, Appli	227	11.8	56.2	24	6	5474828-3	Patent No. 5474828
155	12.2	57.1	29	3	US-09-107-383-3	Sequence 3, Appli	228	11.8	56.2	25	1	US-08-465-590-95	Sequence 95, Appli
156	12.2	57.1	29	4	US-09-643-914-3	Sequence 6, Appli	229	11.8	56.2	25	3	US-08-711-417C-95	Sequence 95, Appli
157	12.2	57.1	30	1	US-08-198-431-6	Sequence 6, Appli	230	11.8	56.2	25	4	US-09-528-115-1	Sequence 1, Appli
158	12.2	57.1	30	1	US-08-564-955-6	Sequence 6, Appli	231	11.8	56.2	25	4	US-09-528-115-2	Sequence 2, Appli
159	12.2	57.1	30	2	US-08-537-874-6	Sequence 6, Appli	232	11.8	56.2	25	4	US-09-528-115-9	Sequence 9, Appli
160	12.2	57.1	30	2	US-08-867-941-46	Sequence 46, Appli	233	11.8	56.2	25	4	US-09-528-115-9	Sequence 9, Appli
161	12.2	57.1	30	2	US-08-867-941-46	Sequence 46, Appli	234	11.8	56.2	25	4	US-09-403-532E-4	Sequence 4, Appli
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163	12.2	57.1	30	3	US-09-100-856A-6	Sequence 6, Appli	236	11.8	56.2	28	2	US-08-356-060A-39	Sequence 39, Appli
164	12.2	57.1	30	3	US-09-075-511-6	Sequence 6, Appli	237	11.8	56.2	28	3	US-08-460-900C-39	Sequence 39, Appli
165	12.2	57.1	30	3	US-09-099-015-6	Sequence 6, Appli	238	11.8	56.2	28	3	US-08-674-509B-39	Sequence 39, Appli
166	12.2	57.1	30	3	US-09-074-658-46	Sequence 46, Appli	239	11.8	56.2	28	3	US-08-954-688-39	Sequence 39, Appli
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168	12.2	57.1	30	3	US-09-133-508A-6	Sequence 6, Appli	241	11.8	56.2	29	4	US-09-639-695-39	Sequence 15, Appli
169	12.2	57.1	30	3	US-09-165-060-6	Sequence 6, Appli	242	11.8	56.2	29	4	US-08-236-886-15	Sequence 15, Appli
170	12.2	57.1	30	3	US-09-501-698-6	Sequence 6, Appli	243	11.8	56.2	30	2	US-09-403-532E-16	Sequence 16, Appli
171	12.2	57.1	30	4	US-08-672-213-34	Sequence 34, Appli	244	11.8	56.2	30	2	US-08-611-757-70	Sequence 70, Appli
172	12.2	57.1	30	4	US-09-240-310-6	Sequence 6, Appli	245	11.8	56.2	30	3	US-08-448-659-1	Sequence 102, App
173	12.2	57.1	30	4	US-09-590-776-6	Sequence 6, Appli	246	11.8	56.2	30	4	US-09-170-496D-102	

C 247	11.8	56.2	30	PCT-US95-05980-70	Sequence 70, Appl	320	11.6	55.2	64	4	US-10-013-784-9	Sequence 9, Appl
C 248	11.8	56.2	32	US-08-305-764C-7	Sequence 7, Appl	321	11.6	55.2	65	3	US-09-415-522-28	Sequence 28, Appl
249	11.8	56.2	33	US-08-456-840-41	Sequence 41, Appl	322	11.6	55.2	66	3	US-08-392-453-45	Sequence 45, Appl
250	11.8	56.2	33	US-08-266-407A-41	Sequence 41, Appl	323	11.6	55.2	66	5	PCT-US91-08525-45	Sequence 45, Appl
251	11.8	56.2	33	US-08-892-544-41	Sequence 41, Appl	324	11.6	55.2	69	1	US-08-220-151-27	Sequence 27, Appl
C 252	11.8	56.2	33	US-09-298-745-2	Sequence 2, Appl	325	11.6	55.2	69	1	US-08-413-118-27	Sequence 27, Appl
C 253	11.8	56.2	33	US-09-474-178-6	Sequence 6, Appl	326	11.6	55.2	69	1	US-08-224-657-4	Sequence 4, Appl
C 254	11.8	56.2	35	US-09-528-271-17	Sequence 17, Appl	327	11.6	55.2	69	1	US-08-257-073-72	Sequence 72, Appl
255	11.8	56.2	41	US-08-860-882A-34	Sequence 34, Appl	328	11.6	55.2	69	2	US-08-184-009-4	Sequence 4, Appl
256	11.8	56.2	41	US-08-860-882A-66	Sequence 66, Appl	329	11.6	55.2	69	2	US-08-486-969-4	Sequence 4, Appl
257	11.8	56.2	41	US-09-011-769A-1	Sequence 1, Appl	330	11.6	55.2	69	2	US-08-417-210A-4	Sequence 4, Appl
C 258	11.8	56.2	41	US-09-011-769A-49	Sequence 49, Appl	331	11.6	55.2	69	2	US-08-458-356-4	Sequence 4, Appl
C 259	11.8	56.2	45	US-08-997-918-2	Sequence 2, Appl	332	11.6	55.2	69	2	US-08-471-024-2	Sequence 4, Appl
260	11.8	56.2	45	US-08-997-918-33	Sequence 33, Appl	333	11.6	55.2	69	3	US-08-473-446-27	Sequence 27, Appl
261	11.8	56.2	47	US-09-641-638-829	Sequence 829, App	334	11.6	55.2	69	3	US-08-460-736-4	Sequence 4, Appl
C 262	11.8	56.2	47	US-09-851-120-2	Sequence 2, Appl	335	11.6	55.2	69	4	US-09-354-138-4	Sequence 4, Appl
C 263	11.8	56.2	47	US-09-422-978-1257	Sequence 1257, Ap	336	11.6	55.2	69	4	US-09-535-370-4	Sequence 4, Appl
C 264	11.8	56.2	48	US-08-477-254A-31	Sequence 31, Appl	337	11.6	55.2	69	5	PCT-US96-00547-4	Sequence 4, Appl
C 265	11.8	56.2	48	US-08-472-576B-31	Sequence 31, Appl	338	11.6	55.2	72	1	US-08-477-877B-70	Sequence 70, Appl
C 266	11.8	56.2	48	US-08-428-734B-31	Sequence 31, Appl	339	11.6	55.2	72	1	US-08-472-281A-70	Sequence 70, Appl
C 267	11.8	56.2	48	US-08-713-556F-31	Sequence 31, Appl	340	11.6	55.2	72	2	US-08-477-989B-70	Sequence 70, Appl
C 268	11.8	56.2	50	US-09-528-271-1	Sequence 1, Appl	341	11.6	55.2	72	2	US-09-301-593-72	Sequence 72, Appl
C 269	11.8	56.2	50	US-09-528-271-2	Sequence 2, Appl	342	11.6	55.2	72	4	US-09-301-593-77	Sequence 77, Appl
C 270	11.8	56.2	50	US-09-528-115-4	Sequence 4, Appl	343	11.6	55.2	75	4	US-08-973-398-9	Sequence 9, Appl
C 271	11.8	56.2	50	US-09-528-115-5	Sequence 5, Appl	344	11.6	55.2	87	2	US-08-631-751A-4	Sequence 4, Appl
C 272	11.8	56.2	51	US-09-528-115-5	Sequence 5, Appl	345	11.6	55.2	97	5	PCT-US94-06456-12	Sequence 12, Appl
C 273	11.8	56.2	64	US-08-153-071-4	Sequence 4, Appl	346	11.6	55.2	97	5	PCT-US94-06456-41	Sequence 41, Appl
C 274	11.8	56.2	64	US-08-609-271-11	Sequence 11, Appl	347	11.6	55.2	98	5	US-08-210-222-22	Sequence 22, Appl
C 275	11.8	56.2	64	US-08-438-511-4	Sequence 4, Appl	348	11.6	55.2	98	5	PCT-US94-06456-20	Sequence 20, Appl
C 276	11.8	56.2	64	US-08-487-431-7	Sequence 7, Appl	349	11.6	55.2	98	5	PCT-US94-06456-49	Sequence 49, Appl
C 277	11.8	56.2	64	US-08-188-374-11	Sequence 11, Appl	350	11.4	54.3	15	2	US-08-585-684B-2073	Sequence 2073, Ap
C 278	11.8	56.2	64	US-08-973-629-7	Sequence 7, Appl	351	11.4	54.3	15	3	US-09-038-073-2073	Sequence 2073, Ap
279	11.8	56.2	65	US-09-482-180A-17	Sequence 17, Appl	352	11.4	54.3	17	5	US-08-308-196A-5	Sequence 5, Appl
C 280	11.8	56.2	76	5314995-6	Patent No. 5314995	353	11.4	54.3	17	5	PCT-US91-06452-5	Sequence 5, Appl
C 281	11.8	56.2	100	US-09-565-241-19	Sequence 19, Appl	354	11.4	54.3	18	2	US-08-174-672D-57	Sequence 57, Appl
C 282	11.6	55.2	25	US-08-477-877B-15	Sequence 15, Appl	355	11.4	54.3	20	2	US-08-616-844-42	Sequence 42, Appl
C 283	11.6	55.2	25	US-08-472-281A-15	Sequence 15, Appl	356	11.4	54.3	20	2	US-08-599-654-42	Sequence 42, Appl
C 284	11.6	55.2	25	US-08-477-989B-15	Sequence 15, Appl	357	11.4	54.3	20	3	US-08-944-868A-42	Sequence 42, Appl
C 285	11.6	55.2	26	US-08-477-877B-82	Sequence 82, Appl	358	11.4	54.3	20	3	US-08-944-423A-42	Sequence 42, Appl
C 286	11.6	55.2	26	US-08-472-281A-82	Sequence 82, Appl	359	11.4	54.3	20	3	US-09-944-446-42	Sequence 42, Appl
C 287	11.6	55.2	26	US-08-477-989B-82	Sequence 82, Appl	360	11.4	54.3	20	3	US-09-313-922-352	Sequence 352, App
C 288	11.6	55.2	30	US-08-349-696-10	Sequence 10, Appl	361	11.4	54.3	20	3	US-09-313-922-352	Sequence 356, App
C 289	11.6	55.2	30	US-08-233-009-10	Sequence 10, Appl	362	11.4	54.3	20	3	US-09-198-442A-6760	Sequence 6760, Ap
C 290	11.6	55.2	30	US-08-560-231-10	Sequence 10, Appl	363	11.4	54.3	22	3	US-09-297-535-5	Sequence 5, Appl
291	11.6	55.2	30	US-08-174-672D-11	Sequence 11, Appl	364	11.4	54.3	22	3	US-09-297-535-6	Sequence 6, Appl
C 292	11.6	55.2	30	US-09-080-704A-10	Sequence 10, Appl	365	11.4	54.3	25	1	US-08-073-807A-14	Sequence 14, Appl
C 293	11.6	55.2	30	US-09-243-560B-8	Sequence 8, Appl	366	11.4	54.3	25	2	US-08-672-814D-6	Sequence 6, Appl
294	11.6	55.2	31	US-08-390-850-219	Sequence 219, App	367	11.4	54.3	25	2	US-09-333-696-6	Sequence 6, Appl
295	11.6	55.2	31	US-08-390-850-220	Sequence 220, App	368	11.4	54.3	25	4	US-09-282-218A-6	Sequence 259, App
296	11.6	55.2	31	US-08-390-850-221	Sequence 221, App	369	11.4	54.3	27	1	US-07-977-284A-259	Sequence 259, App
297	11.6	55.2	31	US-08-390-850-330	Sequence 330, App	370	11.4	54.3	27	1	US-08-599-252-48	Sequence 48, Appl
298	11.6	55.2	31	US-08-390-850-331	Sequence 331, App	371	11.4	54.3	27	1	US-08-647-928-2	Sequence 2, Appl
299	11.6	55.2	31	US-08-390-850-332	Sequence 332, App	372	11.4	54.3	27	2	US-08-256-446B-259	Sequence 259, App
300	11.6	55.2	31	US-08-390-850-333	Sequence 333, App	373	11.4	54.3	27	3	US-09-507-333B-8	Sequence 8, Appl
301	11.6	55.2	31	US-08-435-634-219	Sequence 219, App	374	11.4	54.3	27	5	PCT-US96-06352-48	Sequence 48, Appl
302	11.6	55.2	31	US-08-435-634-220	Sequence 220, App	375	11.4	54.3	27	5	PCT-US96-06352-48	Sequence 48, Appl
303	11.6	55.2	31	US-08-435-634-221	Sequence 221, App	376	11.4	54.3	29	2	US-08-408-774A-5	Sequence 5, Appl
304	11.6	55.2	31	US-08-435-634-330	Sequence 330, App	377	11.4	54.3	29	5	PCT-US96-03792-5	Sequence 5, Appl
305	11.6	55.2	31	US-08-435-634-331	Sequence 331, App	378	11.4	54.3	30	2	US-08-888-366-39	Sequence 39, Appl
306	11.6	55.2	31	US-08-435-634-332	Sequence 332, App	379	11.4	54.3	30	3	US-08-767-128-46	Sequence 46, Appl
307	11.6	55.2	31	US-08-435-634-333	Sequence 333, App	380	11.4	54.3	31	3	US-09-115-468-1	Sequence 1, Appl
C 308	11.6	55.2	32	US-08-712-241-20	Sequence 20, Appl	381	11.4	54.3	31	4	US-09-524-845-1	Sequence 1, Appl
C 309	11.6	55.2	32	US-09-242-131A-6	Sequence 6, Appl	382	11.4	54.3	31	4	US-09-525-258-1	Sequence 1, Appl
C 310	11.6	55.2	32	US-09-615-283-6	Sequence 6, Appl	383	11.4	54.3	31	4	US-09-525-258-1	Sequence 1, Appl
C 311	11.6	55.2	33	US-08-192-300-22	Sequence 22, Appl	384	11.4	54.3	31	4	US-09-525-258-1	Sequence 1, Appl
C 312	11.6	55.2	47	US-09-422-978-690	Sequence 690, App	385	11.4	54.3	33	2	US-08-599-541-142	Sequence 142, App
C 313	11.6	55.2	47	US-09-422-978-1489	Sequence 1489, Ap	386	11.4	54.3	33	2	US-09-124-658-142	Sequence 142, App
C 314	11.6	55.2	47	US-09-422-978-1713	Sequence 1713, Ap	387	11.4	54.3	33	3	US-09-127-460-142	Sequence 142, App
C 315	11.6	55.2	47	US-09-422-978-3112	Sequence 3112, Ap	388	11.4	54.3	33	3	US-08-496-841C-142	Sequence 142, App
C 316	11.6	55.2	49	US-09-647-344A-5	Sequence 5, Appl	389	11.4	54.3	33	3	US-09-124-523-142	Sequence 142, App
C 317	11.6	55.2	53	US-08-388-029A-49	Sequence 49, Appl	390	11.4	54.3	33	4	US-09-636-756A-142	Sequence 142, App
C 318	11.6	55.2	60	5457089-1	Patent No. 5457089	391	11.4	54.3	33	4	US-08-860-882A-16	Sequence 16, Appl
C 319	11.6	55.2	64	US-09-653-403-9	Sequence 9, Appl	392	11.4	54.3	34	2		

C 393	11.4	54.3	34	2	US-08-576-626A-22	Sequence 22, Appl	C 466	11.4	54.3	100	3	US-08-483-577A-119	Sequence 119, App
C 394	11.4	54.3	35	3	US-08-235-836C-87	Sequence 87, Appl	C 467	11.4	54.3	100	4	US-08-897-438-119	Sequence 119, App
C 395	11.4	54.3	36	1	US-08-134-570-16	Sequence 16, Appl	C 468	11.4	54.3	100	4	US-08-637-654-119	Sequence 119, App
C 396	11.4	54.3	36	1	US-09-367-750-5	Sequence 5, Appl	C 469	11.4	54.3	100	4	US-08-649-518-119	Sequence 119, App
C 397	11.4	54.3	36	1	US-09-946-678-25	Sequence 25, Appl	C 470	11.2	53.3	20	4	US-09-651-011A-45	Sequence 45, Appl
C 398	11.4	54.3	37	1	US-08-477-877B-27	Sequence 27, Appl	C 471	11.2	53.3	20	4	US-09-198-452A-6470	Sequence 6470, App
C 399	11.4	54.3	37	1	US-08-472-281A-27	Sequence 27, Appl	C 472	11.2	53.3	21	1	US-08-366-276-7	Sequence 7, Appl
C 400	11.4	54.3	37	2	US-08-477-889B-27	Sequence 27, Appl	C 473	11.2	53.3	22	2	US-08-669-753-2	Sequence 2, Appl
C 401	11.4	54.3	38	3	US-08-686-968C-98	Sequence 98, Appl	C 474	11.2	53.3	22	4	US-09-720-201A-9	Sequence 9, Appl
C 402	11.4	54.3	38	3	US-08-235-836C-90	Sequence 90, Appl	C 475	11.2	53.3	23	4	US-09-629-645A-5	Sequence 5, Appl
C 403	11.4	54.3	39	1	US-08-349-867-1	Sequence 1, Appl	C 476	11.2	53.3	23	4	US-09-297-269-2	Sequence 2, Appl
C 404	11.4	54.3	39	1	US-08-239-476-1	Sequence 1, Appl	C 477	11.2	53.3	24	1	US-08-411-796-194	Sequence 194, App
C 405	11.4	54.3	39	1	US-08-598-305A-1	Sequence 1, Appl	C 478	11.2	53.3	24	1	US-08-411-796-203	Sequence 203, App
C 406	11.4	54.3	39	1	US-08-639-923A-1	Sequence 1, Appl	C 479	11.2	53.3	24	3	US-08-471-039-194	Sequence 194, App
C 407	11.4	54.3	39	2	US-08-732-495-1	Sequence 1, Appl	C 480	11.2	53.3	24	3	US-08-471-039-203	Sequence 203, App
C 408	11.4	54.3	39	2	US-08-686-968C-95	Sequence 95, Appl	C 481	11.2	53.3	24	4	US-08-559-390-194	Sequence 194, App
C 409	11.4	54.3	39	3	US-09-113-750A-20	Sequence 20, Appl	C 482	11.2	53.3	24	4	US-09-331-868A-14	Sequence 14, Appl
C 410	11.4	54.3	39	3	PCT-US95-05431-1	Sequence 1, Appl	C 483	11.2	53.3	24	5	PCT-US93-11198-194	Sequence 203, App
C 411	11.4	54.3	39	5	US-09-626-355-1	Sequence 1, Appl	C 484	11.2	53.3	24	5	PCT-US93-11198-194	Sequence 203, App
C 412	11.4	54.3	41	2	US-08-417-210A-107	Sequence 107, App	C 485	11.2	53.3	25	2	US-08-700-035A-8	Sequence 8, Appl
C 413	11.4	54.3	44	2	US-08-353-400-21	Sequence 21, Appl	C 486	11.2	53.3	25	5	PCT-US96-13457-8	Sequence 8, Appl
C 414	11.4	54.3	44	6	5194376-3	Patent No. 5194376	C 487	11.2	53.3	25	5	US-08-058-299-4	Sequence 4, Appl
C 415	11.4	54.3	45	6	5194376-14	Patent No. 5194376	C 488	11.2	53.3	28	1	US-07-936-163-27	Sequence 27, Appl
C 416	11.4	54.3	45	6	5194376-14	Patent No. 5194376	C 489	11.2	53.3	28	1	US-07-936-163-27	Sequence 27, Appl
C 417	11.4	54.3	47	4	US-09-366-920-7	Sequence 7, Appl	C 490	11.2	53.3	28	2	US-08-482-286A-7	Sequence 7, Appl
C 418	11.4	54.3	47	4	US-09-422-978-1892	Sequence 1892, Ap	C 491	11.2	53.3	28	2	US-08-729-601A-69	Sequence 69, Appl
C 419	11.4	54.3	47	4	US-09-944-243-7	Sequence 7, Appl	C 492	11.2	53.3	29	2	US-08-816-693A-39	Sequence 39, Appl
C 420	11.4	54.3	50	4	US-09-528-271-7	Sequence 7, Appl	C 493	11.2	53.3	29	2	US-08-960-022-26	Sequence 26, Appl
C 421	11.4	54.3	50	4	US-09-528-271-10	Sequence 10, Appl	C 494	11.2	53.3	29	2	US-08-457-254-12	Sequence 12, Appl
C 422	11.4	54.3	51	1	US-08-153-799-1	Sequence 1, Appl	C 495	11.2	53.3	29	3	US-08-885-291-39	Sequence 39, Appl
C 423	11.4	54.3	51	1	US-08-886-967-2	Sequence 2, Appl	C 496	11.2	53.3	29	3	US-08-885-291-39	Sequence 39, Appl
C 424	11.4	54.3	52	3	US-09-307-217-2	Sequence 2, Appl	C 497	11.2	53.3	29	3	US-09-466-672-39	Sequence 39, Appl
C 425	11.4	54.3	52	4	US-08-592-029-6	Sequence 6, Appl	C 498	11.2	53.3	29	5	US-09-304-232-717	Sequence 717, App
C 426	11.4	54.3	54	1	US-08-883-632-6	Sequence 6, Appl	C 499	11.2	53.3	29	5	PCT-US94-08806-24	Sequence 24, Appl
C 427	11.4	54.3	54	2	US-08-592-013A-6	Sequence 6, Appl	C 500	11.2	53.3	30	1	US-07-998-972A-21	Sequence 21, Appl
C 428	11.4	54.3	54	2	US-08-229-379-18	Sequence 18, Appl	C 501	11.2	53.3	30	1	US-08-463-953-21	Sequence 21, Appl
C 429	11.4	54.3	57	1	US-08-701-269-18	Sequence 18, Appl	C 502	11.2	53.3	30	1	US-08-462-261-21	Sequence 21, Appl
C 430	11.4	54.3	66	2	US-08-417-210A-100	Sequence 10, App	C 503	11.2	53.3	30	1	US-08-346-333-3	Sequence 3, Appl
C 431	11.4	54.3	67	2	US-08-464-073-12	Sequence 12, Appl	C 504	11.2	53.3	30	1	US-08-346-333-3	Sequence 3, Appl
C 432	11.4	54.3	67	2	US-08-428-252-12	Sequence 12, Appl	C 505	11.2	53.3	30	2	US-08-746-257A-23	Sequence 23, Appl
C 433	11.4	54.3	67	3	US-08-416-516A-12	Sequence 12, Appl	C 506	11.2	53.3	30	3	US-09-087-312-2	Sequence 2, Appl
C 434	11.4	54.3	75	4	US-09-402-959A-4	Sequence 4, Appl	C 507	11.2	53.3	30	3	US-09-316-080-6	Sequence 6, Appl
C 435	11.4	54.3	81	1	US-08-238-863-37	Sequence 37, Appl	C 508	11.2	53.3	30	4	US-09-534-407-7	Sequence 7, Appl
C 436	11.4	54.3	81	1	US-08-443-407-37	Sequence 37, Appl	C 509	11.2	53.3	30	4	US-09-434-690-3	Sequence 3, Appl
C 437	11.4	54.3	81	1	PCT-US95-05600-181	Sequence 181, App	C 510	11.2	53.3	30	4	US-09-511-964-3	Sequence 3, Appl
C 438	11.4	54.3	81	5	US-09-106-182-16	Sequence 16, App	C 511	11.2	53.3	30	4	US-09-437-687A-3	Sequence 3, Appl
C 439	11.4	54.3	86	4	US-09-227-357-3	Sequence 3, Appl	C 512	11.2	53.3	30	4	US-09-007-288A-98	Sequence 98, Appl
C 440	11.4	54.3	86	4	US-09-280-839-6	Sequence 6, Appl	C 513	11.2	53.3	30	5	PCT-US91-07506-3	Sequence 7, Appl
C 441	11.4	54.3	86	4	US-09-411-977-18	Sequence 18, Appl	C 514	11.2	53.3	30	5	PCT-US91-07506-3	Sequence 4, Appl
C 442	11.4	54.3	86	4	US-09-479-729B-23	Sequence 23, Appl	C 515	11.2	53.3	30	5	PCT-US92-11357-21	Sequence 25, Appl
C 443	11.4	54.3	86	4	US-09-257-179-3	Sequence 3, Appl	C 516	11.2	53.3	31	2	US-08-746-283-25	Sequence 5, Appl
C 444	11.4	54.3	86	4	US-09-149-476-3	Sequence 3, Appl	C 517	11.2	53.3	31	2	US-09-183-217-5	Sequence 17, Appl
C 445	11.4	54.3	86	4	US-09-288-143-3	Sequence 3, Appl	C 518	11.2	53.3	31	3	US-08-064-703-17	Sequence 17, Appl
C 446	11.4	54.3	86	4	US-09-487-792-25	Sequence 25, Appl	C 519	11.2	53.3	32	3	US-08-816-977-28	Sequence 28, Appl
C 447	11.4	54.3	86	4	US-09-152-060-3	Sequence 3, Appl	C 520	11.2	53.3	32	3	US-08-961-083-409	Sequence 409, App
C 448	11.4	54.3	86	4	US-09-908-594-25	Sequence 25, Appl	C 521	11.2	53.3	32	3	US-09-536-784-409	Sequence 1, Appl
C 449	11.4	54.3	86	4	US-09-461-325-3	Sequence 3, Appl	C 522	11.2	53.3	33	1	US-08-152-922A-1	Sequence 1, Appl
C 450	11.4	54.3	86	4	US-09-489-847-3	Sequence 3, Appl	C 523	11.2	53.3	33	1	US-08-157-101A-1	Sequence 1, Appl
C 451	11.4	54.3	86	4	US-09-231-788-18	Sequence 18, Appl	C 524	11.2	53.3	33	1	US-09-345-214-4	Sequence 4, Appl
C 452	11.4	54.3	86	4	US-09-512-363-19	Sequence 19, Appl	C 525	11.2	53.3	33	4	US-09-929-464-4	Sequence 4, Appl
C 453	11.4	54.3	86	4	US-09-176-200-19	Sequence 19, Appl	C 526	11.2	53.3	33	4	US-09-743-980-4	Sequence 19, Appl
C 454	11.4	54.3	86	4	US-09-205-258-3	Sequence 3, Appl	C 527	11.2	53.3	33	4	US-08-049-264C-19	Sequence 19, Appl
C 455	11.4	54.3	86	4	US-09-690-454-3	Sequence 3, Appl	C 528	11.2	53.3	35	1	US-08-476-562-19	Sequence 19, Appl
C 456	11.4	54.3	86	4	US-09-482-271-11	Sequence 11, Appl	C 529	11.2	53.3	35	1	US-08-479-723A-19	Sequence 19, Appl
C 457	11.4	54.3	86	4	US-09-482-273-3	Sequence 3, Appl	C 530	11.2	53.3	35	5	PCT-US94-04310-19	Sequence 19, Appl
C 458	11.4	54.3	86	4	US-09-904-615-3	Sequence 3, Appl	C 531	11.2	53.3	36	1	US-08-347-029-6	Sequence 6, Appl
C 459	11.4	54.3	86	4	US-09-369-247-3	Sequence 3, Appl	C 532	11.2	53.3	36	1	US-08-965-477-2	Sequence 2, Appl
C 460	11.4	54.3	100	1	US-08-487-880A-119	Sequence 119, App	C 533	11.2	53.3	36	4	US-09-129-686-5	Sequence 5, Appl
C 461	11.4	54.3	100	2	US-08-478-435-119	Sequence 119, App	C 534	11.2	53.3	36	4	US-09-566-581-5	Sequence 5, Appl
C 462	11.4	54.3	100	2	US-08-337-463-119	Sequence 119, App	C 535	11.2	53.3	36	5	PCT-US95-14932-6	Sequence 6, Appl
C 463	11.4	54.3	100	2	US-08-478-373-119	Sequence 119, App	C 536	11.2	53.3	37	2	US-08-709-923-6	Sequence 6, Appl
C 464	11.4	54.3	100	2	US-08-478-373-119	Sequence 119, App	C 537	11.2	53.3	37	2	US-08-288-663A-5	Sequence 5, Appl
C 465	11.4	54.3	100	3	US-08-474-671-119	Sequence 119, App	C 538	11.2	53.3	37	2	US-08-288-663A-5	Sequence 5, Appl



C 539	11.2	53.3	37	4	US-09-267-574-35	Sequence 35, Appl	C 612	11.2	53.3	71	3	US-08-471-039-140	Sequence 140, App
C 540	11.2	53.3	38	3	US-08-961-083-415	Sequence 415, App	C 613	11.2	53.3	71	4	US-08-559-390-59	Sequence 59, Appl
C 541	11.2	53.3	38	4	US-09-536-784-415	Sequence 415, App	C 614	11.2	53.3	71	4	US-08-559-390-140	Sequence 140, Appl
C 542	11.2	53.3	39	1	US-07-854-596B-58	Sequence 58, Appl	C 615	11.2	53.3	71	5	PCT-US93-11198-59	Sequence 59, Appl
C 543	11.2	53.3	39	1	US-07-854-596B-59	Sequence 59, Appl	C 616	11.2	53.3	71	5	PCT-US93-11198-140	Sequence 140, App
C 544	11.2	53.3	39	6	5498600-7	Patent No. 5498600	C 617	11.2	53.3	72	4	US-09-120-561C-10	Sequence 10, Appl
C 545	11.2	53.3	40	2	US-08-174-672D-22	Sequence 22, Appl	C 618	11.2	53.3	79	4	US-08-720-01A-10	Sequence 10, Appl
C 546	11.2	53.3	41	1	US-08-279-625A-6	Sequence 6, Appl	C 619	11.2	53.3	81	2	US-08-471-048-9	Sequence 9, Appl
C 547	11.2	53.3	45	2	US-08-432-693-5	Sequence 5, Appl	C 620	11.2	53.3	81	3	US-08-612-85B-5	Sequence 9, Appl
C 548	11.2	53.3	45	2	US-08-642-406A-4	Sequence 4, Appl	C 621	11.2	53.3	81	3	US-08-137-032-9	Sequence 9, Appl
C 549	11.2	53.3	45	4	US-09-199-534-4	Sequence 4, Appl	C 622	11.2	53.3	83	1	US-08-093-741-9	Sequence 9, Appl
C 550	11.2	53.3	45	4	US-09-199-534-4	Sequence 4, Appl	C 623	11.2	53.3	83	1	US-08-093-741-13	Sequence 13, Appl
C 551	11.2	53.3	47	3	US-08-464-582-8	Sequence 8, Appl	C 624	11.2	53.3	83	1	US-08-720-012-9	Sequence 9, Appl
C 552	11.2	53.3	47	3	US-08-464-582-9	Sequence 8, Appl	C 625	11.2	53.3	83	1	US-08-720-012-13	Sequence 13, Appl
C 553	11.2	53.3	47	3	US-08-462-513-8	Sequence 8, Appl	C 626	11.2	53.3	83	2	US-08-560-098A-14	Sequence 14, Appl
C 554	11.2	53.3	47	3	US-08-462-513-9	Sequence 9, Appl	C 627	11.2	53.3	83	3	US-08-967-024C-8	Sequence 8, Appl
C 555	11.2	53.3	47	4	US-09-422-978-2964	Sequence 2964, Ap	C 628	11.2	53.3	84	4	US-09-397-787-13	Sequence 13, Appl
C 556	11.2	53.3	47	4	US-09-422-978-3290	Sequence 3290, Ap	C 629	11.2	53.3	89	1	US-08-411-796-141	Sequence 141, App
C 557	11.2	53.3	48	1	US-08-346-333-7	Sequence 7, Appl	C 630	11.2	53.3	89	1	US-08-411-796-142	Sequence 142, App
C 558	11.2	53.3	48	5	PCT-US91-07506-7	Sequence 7, Appl	C 631	11.2	53.3	89	1	US-08-411-796-143	Sequence 143, App
C 559	11.2	53.3	48	5	PCT-US91-07506-8	Sequence 8, Appl	C 632	11.2	53.3	89	1	US-08-411-796-157	Sequence 157, App
C 560	11.2	53.3	48	5	PCT-US91-07506-8	Sequence 8, Appl	C 633	11.2	53.3	89	1	US-08-411-796-158	Sequence 158, App
C 561	11.2	53.3	49	1	US-07-797-556-10	Sequence 10, Appl	C 634	11.2	53.3	89	1	US-08-411-796-159	Sequence 159, App
C 562	11.2	53.3	50	1	US-08-093-741-24	Sequence 24, Appl	C 635	11.2	53.3	89	3	US-08-471-039-141	Sequence 141, App
C 563	11.2	53.3	50	1	US-08-720-012-24	Sequence 24, Appl	C 636	11.2	53.3	89	3	US-08-471-039-142	Sequence 142, App
C 564	11.2	53.3	50	2	US-08-560-098A-29	Sequence 29, Appl	C 637	11.2	53.3	89	3	US-08-471-039-143	Sequence 143, App
C 565	11.2	53.3	50	3	US-08-967-024C-17	Sequence 17, Appl	C 638	11.2	53.3	89	3	US-08-471-039-157	Sequence 157, App
C 566	11.2	53.3	50	4	US-09-546-934-25	Sequence 25, Appl	C 639	11.2	53.3	89	3	US-08-471-039-158	Sequence 158, App
C 567	11.2	53.3	51	1	US-07-936-163-33	Sequence 33, Appl	C 640	11.2	53.3	89	4	US-08-559-390-141	Sequence 141, App
C 568	11.2	53.3	51	1	US-08-729-601A-80	Sequence 80, Appl	C 641	11.2	53.3	89	4	US-08-559-390-142	Sequence 142, App
C 569	11.2	53.3	51	2	US-08-849-480A-22	Sequence 22, Appl	C 642	11.2	53.3	89	4	US-08-559-390-143	Sequence 143, App
C 570	11.2	53.3	52	2	US-08-411-796-119	Sequence 119, App	C 643	11.2	53.3	89	4	US-08-559-390-157	Sequence 157, App
C 571	11.2	53.3	53	1	US-08-411-796-120	Sequence 120, App	C 644	11.2	53.3	89	4	US-08-559-390-158	Sequence 158, App
C 572	11.2	53.3	53	1	US-08-411-796-121	Sequence 121, App	C 645	11.2	53.3	89	4	US-08-559-390-159	Sequence 159, App
C 573	11.2	53.3	53	1	US-08-411-796-122	Sequence 122, App	C 646	11.2	53.3	89	5	PCT-US93-11198-141	Sequence 141, App
C 574	11.2	53.3	53	1	US-08-411-796-123	Sequence 123, App	C 647	11.2	53.3	89	5	PCT-US93-11198-142	Sequence 142, App
C 575	11.2	53.3	53	1	US-08-411-796-123	Sequence 123, App	C 648	11.2	53.3	89	5	PCT-US93-11198-143	Sequence 143, App
C 576	11.2	53.3	53	3	US-08-471-039-119	Sequence 119, App	C 649	11.2	53.3	89	5	PCT-US93-11198-157	Sequence 157, App
C 577	11.2	53.3	53	3	US-08-471-039-120	Sequence 120, App	C 650	11.2	53.3	89	5	PCT-US93-11198-158	Sequence 158, App
C 578	11.2	53.3	53	3	US-08-471-039-121	Sequence 121, App	C 651	11.2	53.3	89	5	PCT-US93-11198-159	Sequence 159, App
C 579	11.2	53.3	53	3	US-08-471-039-122	Sequence 122, App	C 652	11.2	53.3	90	1	US-08-084-741A-4	Sequence 4, Appl
C 580	11.2	53.3	53	3	US-08-471-039-123	Sequence 123, App	C 653	11.2	53.3	91	1	US-08-093-741-10	Sequence 10, Appl
C 581	11.2	53.3	53	4	US-08-559-390-119	Sequence 119, App	C 654	11.2	53.3	91	1	US-08-093-741-14	Sequence 14, Appl
C 582	11.2	53.3	53	4	US-08-559-390-120	Sequence 120, App	C 655	11.2	53.3	91	1	US-08-720-012-10	Sequence 10, Appl
C 583	11.2	53.3	53	4	US-08-559-390-121	Sequence 121, App	C 656	11.2	53.3	91	1	US-08-720-012-14	Sequence 14, Appl
C 584	11.2	53.3	53	4	US-08-559-390-122	Sequence 122, App	C 657	11.2	53.3	91	2	US-08-560-098A-15	Sequence 15, Appl
C 585	11.2	53.3	53	4	US-08-559-390-123	Sequence 123, App	C 658	11.2	53.3	91	2	US-08-967-024C-9	Sequence 9, Appl
C 586	11.2	53.3	53	5	PCT-US93-11198-119	Sequence 119, App	C 659	11.2	53.3	15	2	US-08-585-684B-2072	Sequence 2072, App
C 587	11.2	53.3	53	5	PCT-US93-11198-120	Sequence 120, App	C 660	11.2	52.4	15	2	US-09-038-073-2072	Sequence 2072, App
C 588	11.2	53.3	53	5	PCT-US93-11198-121	Sequence 121, App	C 661	11.2	52.4	16	2	US-08-771-201-1	Sequence 1, Appl
C 589	11.2	53.3	53	5	PCT-US93-11198-122	Sequence 122, App	C 662	11.2	52.4	17	4	US-09-586-376-14	Sequence 14, Appl
C 590	11.2	53.3	53	5	PCT-US93-11198-123	Sequence 123, App	C 663	11.2	52.4	20	3	US-09-021-701-595	Sequence 595, App
C 591	11.2	53.3	57	2	US-08-612-858-96	Sequence 36, Appl	C 664	11.2	52.4	20	3	US-09-021-701-597	Sequence 597, App
C 592	11.2	53.3	57	2	US-08-560-098A-33	Sequence 33, Appl	C 665	11.2	52.4	21	1	US-08-410-779B-109	Sequence 109, App
C 593	11.2	53.3	58	1	US-08-093-741-18	Sequence 18, Appl	C 666	11.2	52.4	21	1	PCT-US95-04477-109	Sequence 109, App
C 594	11.2	53.3	58	1	US-08-720-012-18	Sequence 18, Appl	C 667	11.2	52.4	21	1	US-08-410-779B-109	Sequence 109, App
C 595	11.2	53.3	58	2	US-08-560-098A-19	Sequence 19, Appl	C 668	11.2	52.4	21	5	US-09-187-793-1	Sequence 1, Appl
C 596	11.2	53.3	58	3	US-08-967-024C-11	Sequence 11, Appl	C 669	11.2	52.4	22	3	US-09-187-793-11	Sequence 11, Appl
C 597	11.2	53.3	58	3	US-09-003-903-4	Sequence 4, Appl	C 670	11.2	52.4	22	3	US-09-305-565B-27	Sequence 27, Appl
C 598	11.2	53.3	58	4	US-09-344-510B-33	Sequence 33, Appl	C 671	11.2	52.4	23	4	US-08-755-587-51	Sequence 51, Appl
C 599	11.2	53.3	60	3	US-08-974-549A-720	Sequence 720, App	C 672	11.2	52.4	24	3	US-08-779-064A-44	Sequence 44, Appl
C 600	11.2	53.3	63	2	US-08-560-098A-37	Sequence 37, Appl	C 673	11.2	52.4	24	4	US-08-812-028-1	Sequence 28, Appl
C 601	11.2	53.3	63	3	US-08-967-024C-22	Sequence 22, Appl	C 674	11.2	52.4	25	1	US-07-971-759-4	Sequence 4, Appl
C 602	11.2	53.3	63	3	US-08-967-024C-23	Sequence 23, Appl	C 675	11.2	52.4	25	2	US-08-211-718-15	Sequence 15, Appl
C 603	11.2	53.3	64	6	5422249-12	Patent No. 5422249	C 676	11.2	52.4	26	3	US-09-187-793-2	Sequence 2, Appl
C 604	11.2	53.3	69	1	US-08-242-098-35	Sequence 35, Appl	C 677	11.2	52.4	26	3	US-09-187-793-3	Sequence 3, Appl
C 605	11.2	53.3	70	1	US-08-093-741-20	Sequence 20, Appl	C 678	11.2	52.4	26	3	US-09-245-041-60	Sequence 60, Appl
C 606	11.2	53.3	70	1	US-08-720-012-20	Sequence 20, Appl	C 679	11.2	52.4	27	1	US-08-197-791-31	Sequence 31, Appl
C 607	11.2	53.3	70	2	US-08-560-098A-21	Sequence 21, Appl	C 680	11.2	52.4	27	3	US-08-909-954-8	Sequence 8, Appl
C 608	11.2	53.3	70	3	US-08-967-024C-13	Sequence 13, Appl	C 681	11.2	52.4	27	3	US-09-081-576-3	Sequence 3, Appl
C 609	11.2	53.3	71	1	US-08-411-796-59	Sequence 59, Appl	C 682	11.2	52.4	28	4	US-09-326-203A-27	Sequence 27, Appl
C 610	11.2	53.3	71	1	US-08-411-796-140	Sequence 140, Appl	C 683	11.2	52.4	29	1	US-08-144-212-4	Sequence 4, Appl
C 611	11.2	53.3	71	3	US-08-471-039-59	Sequence 59, Appl	C 684	11.2	52.4	29	1	US-08-144-212-11	Sequence 11, Appl

C 685	11	52.4	29	1	US-08-105-483-417	Sequence 417, App	C 758	11	52.4	56	3	US-08-928-213B-103	Sequence 103, App
C 686	11	52.4	29	1	US-08-709-209-417	Sequence 417, App	C 759	11	52.4	56	3	US-08-928-213B-104	Sequence 104, App
C 687	11	52.4	29	1	US-08-303-275-125	Sequence 125, App	C 760	11	52.4	60	1	US-08-210-222-37	Sequence 37, App
C 688	11	52.4	29	1	US-08-458-101-417	Sequence 101, App	C 761	11	52.4	60	3	US-08-872-056-10	Sequence 10, App
C 689	11	52.4	29	3	US-08-779-764A-64	Sequence 64, App	C 762	11	52.4	61	3	US-09-046-24-26	Sequence 26, App
C 690	11	52.4	29	4	US-09-851-120-4	Sequence 4, App	C 763	11	52.4	66	1	US-07-977-284A-192	Sequence 192, App
C 691	11	52.4	30	4	US-09-019-793A-108	Sequence 108, App	C 764	11	52.4	66	2	US-08-256-426B-192	Sequence 192, App
C 692	11	52.4	30	4	US-09-860-793-21	Sequence 21, App	C 765	11	52.4	67	2	US-08-464-073-11	Sequence 11, App
C 693	11	52.4	31	2	US-08-577-492-7	Sequence 7, App	C 766	11	52.4	67	2	US-07-814-220-16	Sequence 16, App
C 694	11	52.4	31	2	US-09-079-630-7	Sequence 7, App	C 767	11	52.4	67	2	US-07-814-220-17	Sequence 17, App
C 695	11	52.4	31	2	US-08-859-998-425	Sequence 425, App	C 768	11	52.4	67	2	US-07-812-421-16	Sequence 16, App
C 696	11	52.4	32	2	US-09-925-928-425	Sequence 425, App	C 769	11	52.4	67	2	US-08-428-252-11	Sequence 11, App
C 697	11	52.4	32	4	US-09-225-201B-425	Sequence 425, App	C 770	11	52.4	67	2	US-08-416-516A-11	Sequence 11, App
C 698	11	52.4	33	1	US-08-245-754A-4	Sequence 4, App	C 771	11	52.4	68	3	US-09-081-180-34	Sequence 34, App
C 699	11	52.4	33	1	US-08-485-602-26	Sequence 26, App	C 772	11	52.4	68	3	US-09-040-786-34	Sequence 34, App
C 700	11	52.4	33	1	US-08-757-180-25	Sequence 25, App	C 773	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 701	11	52.4	33	1	US-08-745-638-26	Sequence 26, App	C 774	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 702	11	52.4	33	2	US-08-597-731-4	Sequence 4, App	C 775	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 703	11	52.4	34	1	US-07-955-041-5	Sequence 5, App	C 776	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 704	11	52.4	34	1	US-08-227-455-5	Sequence 5, App	C 777	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 705	11	52.4	34	1	US-08-472-482-5	Sequence 5, App	C 778	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 706	11	52.4	34	1	US-08-487-069-5	Sequence 5, App	C 779	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 707	11	52.4	34	1	US-09-232-477-13	Sequence 13, App	C 780	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 708	11	52.4	34	4	US-09-784-982-13	Sequence 13, App	C 781	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 709	11	52.4	36	1	US-08-316-293-52	Sequence 52, App	C 782	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 710	11	52.4	36	3	US-09-213-053-18	Sequence 18, App	C 783	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 711	11	52.4	38	2	US-08-709-874A-28	Sequence 28, App	C 784	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 712	11	52.4	38	3	US-09-104-382-28	Sequence 28, App	C 785	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 713	11	52.4	39	3	US-09-772-342B-4	Sequence 4, App	C 786	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 714	11	52.4	39	4	US-09-693-147-18	Sequence 18, App	C 787	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 715	11	52.4	40	1	US-08-210-222-39	Sequence 39, App	C 788	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 716	11	52.4	40	3	US-09-306-290-21	Sequence 21, App	C 789	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 717	11	52.4	42	3	US-08-969-815-29	Sequence 29, App	C 790	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 718	11	52.4	42	3	US-09-120-025-29	Sequence 29, App	C 791	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 719	11	52.4	42	4	US-09-710-481-29	Sequence 29, App	C 792	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 720	11	52.4	42	4	US-09-553-875-29	Sequence 29, App	C 793	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 721	11	52.4	42	4	US-09-768-670-29	Sequence 29, App	C 794	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 722	11	52.4	43	1	US-08-210-222-36	Sequence 36, App	C 795	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 723	11	52.4	43	4	US-09-393-007-2	Sequence 2, App	C 796	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 724	11	52.4	44	1	US-08-171-389-129	Sequence 129, App	C 797	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 725	11	52.4	44	1	US-08-123-936-129	Sequence 129, App	C 798	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 726	11	52.4	44	2	US-08-475-228A-129	Sequence 129, App	C 799	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
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C 728	11	52.4	44	3	US-08-482-080A-129	Sequence 129, App	C 801	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
C 729	11	52.4	44	3	US-08-796-101-145	Sequence 145, App	C 802	11	52.4	68	3	US-08-433-126A-73	Sequence 73, App
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## ALIGNMENTS

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RESULT 1
US-08-366-276-8
; Sequence 8, Application US/08366276
; Patent No. 5534409
; GENERAL INFORMATION:
; APPLICANT: Groner, Bernd
; APPLICANT: Gouilleux, Fabrice
; APPLICANT: Wakao, Hiroshi
; TITLE OF INVENTION: Cytokine Regulated Transcription Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,276
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9409396.0
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-19992/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "MGF binding sequence from

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; DESCRIPTION: bovine b-casein"
; HYPOTHETICAL: NO
; US-08-366-276-8

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Best Local Similarity 100.0%; Pred. No. 12;
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; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: Presnell, Julia E.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 100
; TYPE: DNA
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; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12749
; US-09-522-217-59

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Query Match 85.7%; Score 18; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 13;
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QY 1 AGATTCTAGGAATTCAA 18
Db 67 AGATTCTAGGAATTCAA 84

```

```

RESULT 3
US-09-522-217-60/C
; Sequence 60, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024a, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI LIGAND

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FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/09/522,217  
CURRENT FILING DATE: 2000-03-09  
EARLIER APPLICATION NUMBER: US 60/123,547  
EARLIER FILING DATE: 1999-03-09  
EARLIER APPLICATION NUMBER: US 60/123,904  
EARLIER FILING DATE: 1999-03-11  
EARLIER APPLICATION NUMBER: US 60/142,013  
EARLIER FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 100  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC12748  
US-09-522-217-60

Query Match 85.7%; Score 18; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18  
Db 38 AGATTCTAGGAATTCAA 21

## RESULT 4

US-08-369-754-1/c  
Sequence 1, Application US/08369754  
Patent No. 6537553  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, MINORU  
APPLICANT: SAWADA, RITSUKO  
APPLICANT: TSUBOI, SHIGERU  
TITLE OF INVENTION: E-SELECTIN-DEPENDENT CELL ADHESION  
TITLE OF INVENTION: ANTAGONISTS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CAMPBELL AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE. 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/369,754  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1113  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-369-754-1

Query Match 73.3%; Score 15.4; DB 4; Length 24;  
Best Local Similarity 94.1%; Pred. No. 1.8e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATTCTAGCAATTCAA 19  
Db 17 ATTCTAGCAATTCAA 1

## RESULT 5

US-09-140-804-46  
Sequence 46, Application US/09140804  
Patent No. 6197930  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Humes, Jacqueline M.  
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
FILE REFERENCE: 97-49  
CURRENT APPLICATION NUMBER: US/09/140,804  
CURRENT FILING DATE: 1998-08-26  
EARLIER APPLICATION NUMBER: 60/056,983  
EARLIER FILING DATE: 1997-08-26  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 46  
LENGTH: 58  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC14819  
US-09-140-804-46

Query Match 69.5%; Score 14.6; DB 3; Length 58;  
Best Local Similarity 81.0%; Pred. No. 4.2e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAATC 21  
Db 14 AGAATCTAGGAATTCATTC 34

## RESULT 6

US-09-173-043-22  
Sequence 22, Application US/09173043  
Patent No. 6207442  
GENERAL INFORMATION:  
APPLICANT: Raymond, Christopher K.  
TITLE OF INVENTION: PLASMID CONSTRUCTION BY HOMOLOGOUS  
FILE REFERENCE: 97-27  
CURRENT APPLICATION NUMBER: US/09/173,043  
CURRENT FILING DATE: 1998-10-15  
EARLIER APPLICATION NUMBER: US 60/062,061  
EARLIER FILING DATE: 1997-10-16  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 22  
LENGTH: 58  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-173-043-22

Query Match 69.5%; Score 14.6; DB 3; Length 58;  
Best Local Similarity 81.0%; Pred. No. 4.2e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAATC 21  
Db 14 AGAATCTAGGAATTCATTC 34

RESULT 7  
US-09-209-525-42  
Sequence 42, Application US/09209525

```
Patent No. 6303770
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Conklin, Darrell C.
APPLICANT: Parrish, Julia E.
TITLE OF INVENTION: Mammalian Alpha Helical Protein-1
FILE REFERENCE: 97-71
CURRENT APPLICATION NUMBER: US/09/209,525
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 42
LENGTH: 58
TYPE: DNA
ORGANISM: Homo sapiens
US-09-209-525-42

Query Match      69.5%; Score 14.6; DB 4; Length 58;
Best Local Similarity 81.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCGAATC 21
DB 14 AGAATCTAGGAATTCATCTC 34

RESULT 8
US-09-686-838B-46
Sequence 46, Application US/09686838B
Patent No. 6482612
GENERAL INFORMATION:
APPLICANT: Shepard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: Adipocyte-Specific Protein Homologs
FILE REFERENCE: 97-49D1
CURRENT APPLICATION NUMBER: US/09/686,838B
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/140,804
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: US 60/056,983
PRIOR FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46
LENGTH: 58
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide ZC14819
US-09-686-838B-46

Query Match      69.5%; Score 14.6; DB 4; Length 58;
Best Local Similarity 81.0%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCGAATC 21
DB 14 AGAATCTAGGAATTCATCTC 34

RESULT 9
US-09-662-402A-35/c
Sequence 35, Application US/09662402A
Patent No. 6420117
GENERAL INFORMATION:
APPLICANT: Messler, Susan R
APPLICANT: Casa, Alexandra M
TITLE OF INVENTION: MINIATURE INVERTED REPEAT TRANSPOSABLE ELEMENTS AND
FILE REFERENCE: 235.00230101
CURRENT APPLICATION NUMBER: US/09/662,402A
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/153,812
```

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PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-662-402A-35

Query Match      67.6%; Score 14.2; DB 4; Length 20;
Best Local Similarity 84.2%; Pred. No. 6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCGAATC 21
DB 19 ATTCGAGGAATTCGAATC 1

RESULT 10
US-08-201-697-12/c
Sequence 12, Application US/08201697
Patent No. 5705623
GENERAL INFORMATION:
APPLICANT: Miglins, Roger C.
APPLICANT: Thomas, Peedikavil E.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,697
FILING DATE: 25-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UM 9783
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-201-697-12

Query Match      65.7%; Score 13.8; DB 1; Length 30;
Best Local Similarity 88.2%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAA 19
DB 17 AGCTCTAGGAATTCAAA 1

RESULT 11
US-08-463-090B-24/c
```

Sequence 24, Application US/08463090B  
Patent No. 5801015  
GENERAL INFORMATION:  
APPLICANT: Cottarel, Guillaume  
APPLICANT: Damagnez, Veronique  
APPLICANT: Draetta, Gullio  
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from  
NUMBER OF INVENTIONS: Human Pathogens, and Uses Related Thereof  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley, Hoag & Eliot, LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,090B  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.  
REGISTRATION NUMBER: 36,709  
REFERENCE/DOCKET NUMBER: MIV032.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 832-1299  
TELEFAX: (617) 832-7000  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: oligonucleotide  
US-08-463-090B-24

Query Match 65.7%; Score 13.8; DB 1; Length 30;  
Best Local Similarity 88.2%; Pred. No. 9.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAA 19  
DB 20 ATTACTATGAATTCAAA 4

RESULT 12  
US-08-332-420-54/c  
Sequence 54, Application US/08332420  
Patent No. 5744300  
GENERAL INFORMATION:  
APPLICANT: Maarten H. K. Linckens, et al.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR THE  
IDENTIFICATION OF SEQUENCE-RELATED GENES  
NUMBER OF INVENTIONS: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/332,420  
FILING DATE: October 31, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/235,180  
FILING DATE: April 29, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Waidburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-332-420-54

Query Match 64.8%; Score 13.6; DB 1; Length 34;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20  
DB 32 AGAGATCGAAGATTCAAAT 13

RESULT 13  
US-07-941-363-1  
Sequence 1, Application US/07941363  
Patent No. 5348886  
GENERAL INFORMATION:  
APPLICANT: Lee, Stephen C.  
APPLICANT: Luckow, Verne A.  
APPLICANT: Leusch, Mark S.  
APPLICANT: Olin, Peter O.  
TITLE OF INVENTION: Method of Producing Recombinant  
Eukaryotic Viruses in Bacteria  
NUMBER OF INVENTIONS: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG  
STREET: 800 N. Lindbergh Blvd.  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63167  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/941,363  
FILING DATE: 19920904  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: 07-21 (872) A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 694-5402  
TELEFAX: (314) 694-9009  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)



US-07-941-363-1

Query Match 64.8%; Score 13.6; DB 1; Length 37;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20  
DB 1 AGATTCTAGGAATTCACAT 20

RESULT 14

US-09-143-634-28/c

Sequence 28, Application US/09143634  
Patent No. 6214602  
GENERAL INFORMATION:  
APPLICANT: Zdanovsky, Alexey G.  
TITLE OF INVENTION: EXPRESSION OF CLOSTRIDIAL TOXINS AND PROTEINS  
FILE REFERENCE: PRMG-03193  
CURRENT APPLICATION NUMBER: US/09/143,634  
CURRENT FILING DATE: 1998-08-28  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 28  
LENGTH: 38  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-143-634-28

Query Match 64.8%; Score 13.6; DB 3; Length 38;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GATTTCAGGAATTCAAATC 21  
DB 21 GATTTCAGGAATTCAGATC 2

RESULT 15

US-08-308-196A-4

Sequence 4, Application US/08308196A  
Patent No. 5612198  
GENERAL INFORMATION:  
APPLICANT: Briereley, Russell A.  
APPLICANT: Davis, Geneva R.  
APPLICANT: Holtz, Gregory C.  
APPLICANT: Gleeson, Martin A.  
APPLICANT: Howard, Bradley D.  
TITLE OF INVENTION: Production of Insulin-Like Growth  
Factor-1 in Methylotrophic Yeast Cells  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brown, Martin, Haller & McClain  
STREET: 1660 Union Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-2926  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/308,196A  
FILING DATE: 09-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,523  
FILING DATE: 03-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/578,728

FILING DATE: 04-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 51875

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic DNA)

US-08-308-196A-4

Query Match 64.8%; Score 13.6; DB 1; Length 40;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20  
DB 5 AGCTTGATAGGAATTCAAAT 24

RESULT 16

US-09-289-803-3

Sequence 3, Application US/09289803  
Patent No. 6162605  
GENERAL INFORMATION:  
APPLICANT: Fort, Thomas L.  
APPLICANT: McMillian, Ray A.  
APPLICANT: Hellyer, Tobin  
APPLICANT: You, Oimlin  
TITLE OF INVENTION: Amplification and Detection of Shiga-Like Toxin I  
FILE REFERENCE: SLT-1 Application  
CURRENT APPLICATION NUMBER: US/09/289,803  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 3  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Primer for SDA  
US-09-289-803-3

Query Match 64.8%; Score 13.6; DB 3; Length 40;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20  
DB 13 AGACTTCTCGGAATTCACAT 32

RESULT 17

PCT-US91-06452-4

Sequence 4, Application PC/TUS9106452  
GENERAL INFORMATION:  
APPLICANT: Briereley, Russell A.  
APPLICANT: Davis, Geneva R.  
APPLICANT: Holtz, Gregory C.  
APPLICANT: Gleeson, Martin A.  
APPLICANT: Bradley, D. H.  
TITLE OF INVENTION: Production of Insulin-Like Growth  
Factor-1 in Methylotrophic Yeast Cells  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:

ADDRESSER: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/06452  
FILING DATE: 19910409  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/578,728  
FILING DATE: 04-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 51874  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
TELEFAX: (619)552-0095  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
PCT-US91-06452-4

Query Match 64.8%; Score 13.6; DB 5; Length 40;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20  
DB 5 AGCTTGATAGGAATTCAAAT 24

RESULT 18  
US-09-289-803-2  
Sequence 2, Application US/09289803  
Patent No. 6162605  
GENERAL INFORMATION:  
APPLICANT: Fort, Thomas L.  
APPLICANT: McMillian, Ray A.  
APPLICANT: Hellyer, Tobin  
APPLICANT: You, Qimin  
TITLE OF INVENTION: Amplification and Detection of Shiga-like Toxin I  
FILE REFERENCE: SLT-I Producing Organisms  
CURRENT APPLICATION NUMBER: US/09/289,803  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 41  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Primer for SDA  
OTHER INFORMATION: of SLT-I Producing Organisms  
US-09-289-803-2

Query Match 64.8%; Score 13.6; DB 3; Length 41;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20

DB 13 AGACTTCGCGAATTCACAT 32

RESULT 19  
US-09-289-803-1  
Sequence 1, Application US/09289803  
Patent No. 6162605  
GENERAL INFORMATION:  
APPLICANT: Fort, Thomas L.  
APPLICANT: McMillian, Ray A.  
APPLICANT: Hellyer, Tobin  
APPLICANT: You, Qimin  
TITLE OF INVENTION: Amplification and Detection of Shiga-like Toxin I  
FILE REFERENCE: SLT-I Application  
CURRENT APPLICATION NUMBER: US/09/289,803  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:Primer for SDA  
OTHER INFORMATION: of SLT-I Producing Organisms  
US-09-289-803-1

Query Match 64.8%; Score 13.6; DB 3; Length 42;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20  
DB 13 AGACTTCGCGAATTCACAT 32

RESULT 20  
5221737-7  
Patent No. 5221737  
APPLICANT: BARTSCH, KLAUS;SCHULZ, ARNO;UHLMANN, EUGEN  
TITLE OF INVENTION: GENE AND GENE STRUCTURE CODING FOR AN  
AMINOTRANSFERASE, AND MICROORGANISMS WHICH EXPRESS THIS GENE  
NUMBER OF SEQUENCES: 12  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US//07/450,230  
FILING DATE: 13-DEC-1989  
SEQ ID NO: 7;  
LENGTH: 68  
5221737-7

Query Match 64.8%; Score 13.6; DB 6; Length 68;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAAT 20  
DB 4 AGATTACTAGGAATTCAAAT 23

RESULT 21  
US-09-030-613-30  
Sequence 30, Application US/09030613  
Patent No. 6083706  
GENERAL INFORMATION:  
APPLICANT: Florckiewicz, Robert Z.  
APPLICANT: Baird, V. Andrew  
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/030,613  
FILING DATE: 25-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6083706tendburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 760100.41BCL  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-030-613-30

Query Match 63.8%; Score 13.4; DB 3; Length 30;  
Best Local Similarity 93.3%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTAGGAATTCAATC 21  
Db 1 CTAGGAATTCAATC 15

RESULT 22  
US-09-451-905-30  
Sequence 30, Application US/09451905  
PATENT No. 6306613  
GENERAL INFORMATION:  
APPLICANT: Robert Z. Flokiewicz  
APPLICANT: Andrew Baird  
APPLICANT: Dale E. Warnock  
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME  
FILE REFERENCE: 200124.402C4  
CURRENT APPLICATION NUMBER: US/09/451,905  
CURRENT FILING DATE: 1999-12-01  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: PCR Primer  
US-09-451-905-30

Query Match 63.8%; Score 13.4; DB 4; Length 30;  
Best Local Similarity 93.3%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTAGGAATTCAATC 21  
Db 1 CTAGGAATTCAATC 15

RESULT 23  
US-09-313-221A-77  
Sequence 77, Application US/09313221A  
Patent No. 6468743

GENERAL INFORMATION:  
APPLICANT: Thomas L. Romick (Inventor)  
APPLICANT: Mark S. Fraser (Inventor)  
TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL  
TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS  
FILE REFERENCE: HUNT-042784  
CURRENT APPLICATION NUMBER: US/09/313,221A  
CURRENT FILING DATE: 1999-05-17  
PRIOR APPLICATION NUMBER: US 60/086,025  
PRIOR FILING DATE: 1998-05-18  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 77  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Staphylococcus aureus  
US-09-313-221A-77

Query Match 63.8%; Score 13.4; DB 4; Length 40;  
Best Local Similarity 93.3%; Pred. No. 1.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CTAGGAATTCAATC 21  
Db 11 CTAGGAATTCAATC 25

RESULT 24  
US-08-840-316-5/c  
Sequence 5, Application US/08840316  
PATENT No. 6054567  
GENERAL INFORMATION:  
APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,  
APPLICANT: Tsarev, Sergei, A., and Robinson, Robin A.  
TITLE OF INVENTION: Recombinant Proteins Of  
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/840,316  
FILING DATE: 11-APR-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard W. Bork  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4255  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-840-316-5

Query Match 62.9%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATTCTAGGAATCAAT 20  
Db 20 ATGCTGTGAATCAAT 3

RESULT 25  
US-08-809-523-5/c  
; Sequence 5, Application US/08809523  
; Patent No. 6207416  
; GENERAL INFORMATION:  
; APPLICANT: Tsarev, Sergei. A., Emerson,  
; APPLICANT: Suzanne U., Purcell, Robert H.  
; TITLE OF INVENTION: Recombinant Proteins Of  
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their  
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,523  
; FILING DATE: 28-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13102  
; FILING DATE: 03-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US08/316,765  
; FILING DATE: 03-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/947,263  
; FILING DATE: 18-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Richard W. Bork  
; REGISTRATION NUMBER: 36,459  
; REFERENCE/DOCKET NUMBER: 2026-4032US4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-809-523-5

Query Match 62.9%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATTCTAGGAATCAAT 20  
Db 20 ATGCTGTGAATCAAT 3

RESULT 26  
US-08-471-971-5/c  
; Sequence 5, Application US/08471971  
; Patent No. 6287759  
; GENERAL INFORMATION:

APPLICANT: Tsarev, Sergei. A., Emerson,  
APPLICANT: Suzanne U., Purcell, Robert H.  
TITLE OF INVENTION: Recombinant Proteins Of  
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their  
TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,971  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US08/316,765  
FILING DATE: 03-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US07/947,263  
FILING DATE: 18-SEP-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Richard W. Bork  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4032US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-471-971-5

Query Match 62.9%; Score 13.2; DB 3; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 ATTCTAGGAATCAAT 20  
Db 20 ATGCTGTGAATCAAT 3

RESULT 27  
US-09-402-776-5/c  
; Sequence 5, Application US/09402776  
; Patent No. 6458562  
; GENERAL INFORMATION:  
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,  
; APPLICANT: Tsarev, Sergei. A., and Robinson, Robin A.  
; TITLE OF INVENTION: Recombinant Proteins Of  
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their  
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/840,316
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-402-776-5

Query Match          62.9%; Score 13.2; DB 4; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAAT 20
DB 20 ATGCTGTGATTCAAAT 3

RESULT 28
PCT-US93-08849A-5/c
; Sequence 5, Application PC/TUS9308849A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08849A
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William S. Feiler
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4032 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
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```

; STRANDEDNESS: single
; TOPOLOGY: linear
;
PCT-US93-08849A-5

Query Match          62.9%; Score 13.2; DB 5; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAAT 20
DB 20 ATGCTGTGATTCAAAT 3

RESULT 29
PCT-US93-08849-5/c
; Sequence 5, Application PC/TUS9308849
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08849
; FILING DATE: 17-SEP-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bork, Richard, W.
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
PCT-US93-08849-5

Query Match          62.9%; Score 13.2; DB 5; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAAT 20
DB 20 ATGCTGTGATTCAAAT 3

RESULT 30
US-09-182-816-30/c
; Sequence 30, Application US/09182816
; Patent No. 6143542
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
```

APPLICANT: Silver, Gary M.  
APPLICANT: Lo, Katherine C.  
APPLICANT: Brandt, Kevin S.  
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,  
FILE REFERENCE: FC-3-C1  
CURRENT APPLICATION NUMBER: US/09/182,816  
CURRENT FILING DATE: 1998-10-29  
EARLIER FILING DATE: 1997-12-12  
EARLIER APPLICATION NUMBER: 08/989,510  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Primer  
US-09-182-816-30

Query Match 62.9%; Score 13.2; DB 3; Length 31;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTGAGATTCAA 18  
Db 19 AGATCTCTGAGATTCAA 2

## RESULT 31

US-09-471-528-30/C  
Sequence 30, Application US/09471528  
Patent No. 6153397  
GENERAL INFORMATION:  
APPLICANT: Wisniewski, Nancy  
APPLICANT: Silver, Gary M.  
APPLICANT: Lo, Katherine C.  
APPLICANT: Brandt, Kevin S.  
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF  
FILE REFERENCE: FC-3-C1-1  
CURRENT APPLICATION NUMBER: US/09/471,528  
CURRENT FILING DATE: 1999-12-27  
EARLIER APPLICATION NUMBER: 09/182,816  
EARLIER FILING DATE: 1998-10-29  
EARLIER APPLICATION NUMBER: 08/989,510  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Primer  
US-09-471-528-30

Query Match 62.9%; Score 13.2; DB 3; Length 31;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTGAGATTCAA 18  
Db 19 AGATCTCTGAGATTCAA 2

RESULT 32  
US-09-634-530-30/C  
Sequence 30, Application US/09634530  
Patent No. 6290958  
GENERAL INFORMATION:  
APPLICANT: Wisniewski, Nancy

APPLICANT: Silver, Gary M.  
APPLICANT: Lo, Katherine C.  
APPLICANT: Brandt, Kevin S.  
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND USES THEREOF  
FILE REFERENCE: FC-3-C1-1  
CURRENT APPLICATION NUMBER: US/09/634,530  
CURRENT FILING DATE: 2000-08-08  
PRIOR APPLICATION NUMBER: 09/471,528  
PRIOR FILING DATE: 1999-12-27  
PRIOR APPLICATION NUMBER: 09/182,816  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 08/989,510  
PRIOR FILING DATE: 1997-12-12  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Primer  
US-09-634-530-30

Query Match 62.9%; Score 13.2; DB 3; Length 31;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTGAGATTCAA 18  
Db 19 AGATCTCTGAGATTCAA 2

## RESULT 33

US-07-955-041-6/C  
Sequence 6, Application US/07955041  
Patent No. 5360733  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, MINORU  
APPLICANT: BIERHUIZEN, MARTI FA  
TITLE OF INVENTION: A NOVEL BETAL-6  
TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTANSFERASE, ITS ACCEPTOR MOLECULE,  
TITLE OF INVENTION: LEUKOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: CAMPBELL AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/955,041  
FILING DATE: 19921001  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATRYN  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-07-955-041-6

Query Match 62.9%; Score 13.2; DB 1; Length 33;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATTCAAA 19  
DB 18 GGTTCTCGCAATTCAAA 1

RESULT 34  
US-08-227-455-6/c  
Sequence 6, Application US/08227455

PATENT No. 5624832  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, MINORU  
APPLICANT: BIERHUIZEN, MARTI FA  
TITLE OF INVENTION: A NOVEL BETA1-6  
TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTRANSFERASE, ITS ACCEPTOR MOLECULE,  
TITLE OF INVENTION: LEUKOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING  
TITLE OF INVENTION: ENZYMAITC ACTIVITY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CAMPBELL AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/227,455  
FILING DATE: 14-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9957  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-227-455-6  
Query Match 62.9%; Score 13.2; DB 1; Length 33;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATTCAAA 19  
DB 18 GGTTCTCGCAATTCAAA 1

RESULT 35  
US-08-472-482-6/c  
Sequence 6, Application US/08472482

PATENT No. 5658778  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, MINORU  
APPLICANT: BIERHUIZEN, MARTI FA

TITLE OF INVENTION: A NOVEL BETA1-6  
TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTRANSFERASE, ITS ACCEPTOR MOLECULE,  
TITLE OF INVENTION: LEUKOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING  
TITLE OF INVENTION: ENZYMAITC ACTIVITY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CAMPBELL AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,482  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/955,041

FILING DATE: 01-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATHRYN

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 9294

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-9001

TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-472-482-6

Query Match 62.9%; Score 13.2; DB 1; Length 33;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATTCAAA 19  
DB 18 GGTTCTCGCAATTCAAA 1

RESULT 36  
US-08-487-069-6/c  
Sequence 6, Application US/08487069

PATENT No. 5684134  
GENERAL INFORMATION:  
APPLICANT: FUKUDA, MINORU  
APPLICANT: BIERHUIZEN, MARTI FA  
TITLE OF INVENTION: A NOVEL BETA1-6  
TITLE OF INVENTION: N-ACETYLGLUCOSAMINYLTRANSFERASE, ITS ACCEPTOR MOLECULE,  
TITLE OF INVENTION: LEUKOSIALIN AND A METHOD FOR CLONING PROTEINS HAVING  
TITLE OF INVENTION: ENZYMAITC ACTIVITY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CAMPBELL AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25



CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,069  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/955,041  
FILING DATE: 01-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHERYN  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-487-069-6

Query Match 62.9%; Score 13.2; DB 1; Length 33;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GATTCTAGGAATTCATA 19  
DB 18 GATTCTGCGAATTCATA 1

RESULT 37  
US-08-169-715-47/c  
Sequence 47, Application US/08169715  
Patent No. 6300056  
GENERAL INFORMATION:  
APPLICANT: Irvine, Bruce D.  
APPLICANT: Horn, Thomas  
APPLICANT: Chang, Chu-An  
TITLE OF INVENTION: HIV PROBS FOR USE IN SOLUTION PHASE  
TITLE OF INVENTION: SANDWICH HYBRIDIZATION ASSAYS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,715  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/813,583  
FILING DATE: 18-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 22300-20150.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-813-5600  
TELEFAX: 415-327-2951  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-169-715-47

Query Match 62.9%; Score 13.2; DB 4; Length 33;  
Best Local Similarity 60.0%; Pred. No. 1.8e+03;  
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCATA 20  
DB 28 GATTCTGCGAATTCATA 9

RESULT 38  
US-09-140-804-38  
Sequence 38, Application US/09140804  
Patent No. 6197930  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Humes, Jacqueline M.  
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
FILE REFERENCE: 97-49  
CURRENT APPLICATION NUMBER: US/09/140,804  
CURRENT FILING DATE: 1998-08-26  
EARLIER APPLICATION NUMBER: 60/056,983  
EARLIER FILING DATE: 1997-08-26  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 38  
LENGTH: 63  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC15223  
US-09-140-804-38

Query Match 62.9%; Score 13.2; DB 3; Length 63;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCATA 18  
DB 46 AGAATCTAGGAATTCATA 63

RESULT 39  
US-09-686-838B-38  
Sequence 38, Application US/09686838B  
Patent No. 6482612  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Humes, Jacqueline M.  
TITLE OF INVENTION: Adipocyte-Specific Protein Homologs  
FILE REFERENCE: 97-49D1  
CURRENT APPLICATION NUMBER: US/09/686,838B  
CURRENT FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 09/140,804  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: US 60/056,983  
PRIOR FILING DATE: 1997-08-26  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 63  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC15223  
US-09-686-838B-38  
Query Match 62.9%; Score 13.2; DB 4; Length 63;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 12:00:17 ; Search time 126.318 Seconds

(without alignments)  
448.773 Million cell updates/sec

Title: US-09-744-875a-1

Perfect score: 21

Sequence: 1 agattctcaggaattcaatc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2722628

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
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2: /SIDS1/gcgdata/geneeq/geneeqn-emb1/NA1981.DAT:\*  
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12: /SIDS1/gcgdata/geneeq/geneeqn-emb1/NA1991.DAT:\*  
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14: /SIDS1/gcgdata/geneeq/geneeqn-emb1/NA1993.DAT:\*  
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24: /SIDS1/gcgdata/geneeq/geneeqn-emb1/NA2002.DAT:\*  
25: /SIDS1/gcgdata/geneeq/geneeqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	21	21	AAZ92037	STARTS binding sequ
2	18	85.7	20	AAV46012	Immunis adjuvant ST
3	18	85.7	20	AAI39155	Murine Toli-like r
4	18	85.7	21	ABT17264	Transcription fact
5	18	85.7	21	ABT17265	Transcription fact
6	18	85.7	63	ABT17327	Transcription fact
7	18	85.7	100	AAA54479	DNA fragment compr
8	18	85.7	100	AAA54480	DNA fragment compr

9	18	85.7	100	24	ABA93801	KZ134 plasmid cons
10	18	85.7	100	24	ABA93802	KZ134 plasmid cons
11	18	85.7	100	24	AAZ20691	Plasmid K2 134 oli
12	18	85.7	100	24	AAZ20692	Plasmid K2 134 oli
13	18	85.7	100	24	AAZ22953	BAF3/KZ134/zalpal
14	18	85.7	100	24	AAZ22954	BAF3/KZ134/zalpal
15	16	76.2	33	24	ABK88204	Human cytochrome b
16	15.4	73.3	51	22	AAI31609	Human SNP oligonc
17	14.8	70.5	41	24	ABL53039	Oligonucleotide JC
18	14.8	70.5	41	24	ABL53041	Oligonucleotide JC
19	14.8	70.5	44	24	ABL53037	Oligonucleotide JC
20	14.8	70.5	44	24	ABL53043	Oligonucleotide JC
21	14.6	69.5	46	20	AAZ23234	HCV NS5B gene ampl
22	14.6	69.5	58	19	AAV59344	zeig10 primer ZC15
23	14.6	69.5	58	20	AAV80718	primer-5 for C-ter
24	14.6	69.5	58	22	AAV24706	Linker primer ZC14
25	14.6	69.5	58	22	AAV00972	PCR antisense comm
26	14.6	69.5	58	24	ABN83120	Human alpha helica
27	14.6	69.5	58	24	ABK12090	C-terminal-CRE-Zal
28	14.2	67.6	20	24	ABV72202	Nucleotide sequenc
29	14.2	67.6	27	22	AAI64395	PCR primer #2. Un
30	14.2	67.6	27	22	AAI64405	PCR primer #12. U
31	14.2	67.6	61	21	AAI76494	Human silent SNP c
32	14.2	67.6	61	21	AAV52964	Arabidopsis thaila
33	14.2	67.6	81	18	AAI76363	C. krusei non-tran
34	14	66.7	60	24	ABN41529	Human spliced tran
35	13.8	65.7	30	18	AAI58221	Candida CBI gene
36	13.8	65.7	30	21	AAV04870	PCR primer 2 used
37	13.8	65.7	30	19	AAZ08279	PCR primer-1 used
38	13.8	65.7	60	24	ABN47639	Human spliced tran
39	13.8	65.7	65	24	ABN57384	Mouse spliced tran
40	13.6	64.8	22	13	AAQ32872	Human apolipoprote
41	13.6	64.8	30	16	AAQ87051	Apolipoprotein B 9
42	13.6	64.8	30	24	ABX6781	Novel Helicobacter
43	13.6	64.8	34	17	AAI28097	Probe 0711 isolate
44	13.6	64.8	37	15	AAQ73305	Mini-actin7 primer
45	13.6	64.8	37	16	AAQ86761	attn7 amplificati
46	13.6	64.8	38	21	AAZ95731	Clostridium botuli
47	13.6	64.8	40	21	AAQ63106	Shiga-like toxin I
48	13.6	64.8	41	21	AAQ63105	Shiga-like toxin I
49	13.6	64.8	42	21	AAQ63104	Shiga-like toxin I
50	13.6	64.8	44	24	AAZ29413	PCR primer to crea
51	13.6	64.8	48	17	AAI76834	Primer p2 for apol
52	13.6	64.8	51	22	AAI30344	Human SNP oligonc
53	13.6	64.8	51	22	AAI73799	Human SNP oligonc
54	13.6	64.8	52	21	AAI31226	AAR target oligonc
55	13.4	63.8	28	24	ABK69051	Human alpha relate
56	13.4	63.8	30	19	AAV60355	Reverse PCR primer
57	13.4	63.8	30	21	AAV55582	Reverse primer for
58	13.4	63.8	30	24	AAI517419	HIV Transactivatin
59	13.4	63.8	33	22	AAH73718	Sodium neurotran
60	13.4	63.8	40	21	AAZ46392	Primer specific fo
61	13.4	63.8	42	22	AAZ27320	PCR primer, SEQ ID
62	13.4	63.8	42	20	AAZ29922	PCR primer MLI1 us
63	13.4	63.8	65	24	ABN55578	Mouse spliced tran
64	13.2	62.9	25	15	AAQ45198	HEV strain BUR-121
65	13.2	62.9	25	17	AAI27395	HEV strain Burma-1
66	13.2	62.9	25	19	AAV71605	HEV ORF proteins e
67	13.2	62.9	28	17	AAI38378	Streptomyces avidi
68	13.2	62.9	31	20	AAV86298	PCR primer used to
69	13.2	62.9	31	22	AAI66767	Flea epoxide hydro
70	13.2	62.9	31	22	AAV91984	Primer newBExpant
71	13.2	62.9	31	22	AAQ86298	HIV capture probe
72	13.2	62.9	33	14	AAQ6745	Sequence of PCR pr
73	13.2	62.9	33	16	AAQ61561	Human immunodefici
74	13.2	62.9	33	22	AAQ89521	C parvum P21 prote
75	13.2	62.9	36	15	AAQ74777	Phaenolocooccus epi
76	13.2	62.9	36	15	AAQ74777	Candida essential
77	13.2	62.9	43	24	ABZ25932	ZNF158 breakpoint
78	13.2	62.9	48	20	AAV87186	ZNF158-FGFR1 trans
79	13.2	62.9	48	24	AAV87188	Human leukocyte ge
80	13.2	62.9	50	20	ABZ08121	myc-SRKDEL encodin
81	13.2	62.9	60	22	AAI10085	

C	82	13.2	62.9	60	24	ABN44100	Human spliced tran
C	83	13.2	62.9	63	24	AAK24698	Linker primer ZC15
C	84	13.2	62.9	65	24	ABZ28545	Candida gene relat
C	85	13.2	62.9	72	16	AAAT01456	PCR primer GHVp79
C	86	13.2	62.9	78	24	ABN68040	B-domain-deleted-F
C	87	13	61.9	20	24	ABN85827	Related to Bombyx
C	88	13	61.9	21	17	AAAT32884	HTV-II gag p19 pr
C	89	13	61.9	21	17	AAAT29265	HTV-II gag p19 pr
C	90	13	61.9	22	25	ACA58182	Human familial b1p
C	91	13	61.9	23	25	AAAD92226	Mouse phospholipid
C	92	13	61.9	26	16	AAAT04521	Human LBP (1-197) p
C	93	13	61.9	26	24	ABT04461	Human G-protein co
C	94	13	61.9	26	24	ABT04464	Human G-protein co
C	95	13	61.9	26	24	ABT04467	Human G-protein co
C	96	13	61.9	26	24	ABT04470	Human G-protein co
C	97	13	61.9	26	24	ABL92840	G protein-coupled
C	98	13	61.9	26	24	ABL92843	G protein-coupled
C	99	13	61.9	27	17	AAAT29257	C. difficile toxin
C	100	13	61.9	27	19	AAV30566	Clostridium diffic
C	101	13	61.9	33	24	ABN57048	Human natriferetic
C	102	13	61.9	35	17	AAAT12411	Soluble human eyt
C	103	13	61.9	40	17	AAAT33879	Human PKR12 codin
C	104	13	61.9	50	21	AAAT5084	Oligonucleotide us
C	105	13	61.9	50	21	AAAD00190	Oligo BET-104 to g
C	106	13	61.9	50	24	ABZ02216	Human leukocyte ge
C	107	13	61.9	50	24	ABZ03732	Human leukocyte ge
C	108	13	61.9	51	25	ABZ77469	PCR primer for a t
C	109	13	61.9	65	24	ABN58474	Mouse spliced tran
C	110	13	61.9	85	19	AAV21703	Thrombopoietin exp
C	111	13	61.9	85	19	AAV21704	Thrombopoietin exp
C	112	13	61.9	96	16	AAO80989	HIV protease inh
C	113	13	61.9	96	16	AAO80986	HIV protease inh
C	114	13	61.9	96	21	AACT2049	Human secreted pro
C	115	13	61.9	96	21	AACT2049	Tumour suppression
C	116	12.8	61.0	17	25	ABT38567	Yeast cAMP-depende
C	117	12.8	61.0	28	17	AAAT32202	Primer 3'C, amplif
C	118	12.8	61.0	30	15	AAQ72219	Human alpha-1C adr
C	119	12.8	61.0	30	22	AAAD1604	Staphylococcus aur
C	120	12.8	61.0	30	22	AAAD1632	Human PACE PCR pri
C	121	12.8	61.0	32	20	AAAS03316	Primer for humanis
C	122	12.8	61.0	32	20	AAAX08584	Human PCR primer h
C	123	12.8	61.0	33	24	AAAT19064	PCR primer for C.
C	124	12.8	61.0	34	21	AAAT43241	Rop fusion randoml
C	125	12.8	61.0	36	21	AAAS6078	C. perfringens end
C	126	12.8	61.0	42	22	AAAT1834	BGH transcription
C	127	12.8	61.0	43	17	AAAT30815	BGH transcription
C	128	12.8	61.0	43	18	AAAX5253	Reverse PCR primer
C	129	12.8	61.0	43	19	AAV60152	Reverse PCR primer
C	130	12.8	61.0	43	19	AAV42352	BGH transcription
C	131	12.8	61.0	43	20	AAAX58505	Reverse primer BGH
C	132	12.8	61.0	43	21	AAAT70712	Bovine growth horn
C	133	12.8	61.0	43	21	AAAT29268	Bovine growth horn
C	134	12.8	61.0	43	21	AAAT38808	Alphavirus related
C	135	12.8	61.0	43	24	ABK46274	Bovine growth horn
C	136	12.8	61.0	43	25	ABK81462	Bovine growth horn
C	137	12.8	61.0	50	24	ABZ04055	Human leukocyte ge
C	138	12.8	61.0	50	24	AAV49468	Signal sequence fo
C	139	12.8	61.0	60	24	ABN43043	Human spliced tran
C	140	12.8	61.0	60	24	ABN46682	Human spliced tran
C	141	12.8	61.0	61	21	AAAC69885	VEGF-binding nucle
C	142	12.8	61.0	61	21	AAAC69887	VEGF-binding nucle
C	143	12.8	61.0	65	24	ABZ27088	Candida essential
C	144	12.8	61.0	65	24	ABZ28178	Candida gene relat
C	145	12.8	61.0	65	24	ABN29091	Rat spliced transc
C	146	12.8	61.0	67	13	AAO36987	VLI, Ox VL 5'-end
C	147	12.8	61.0	83	22	AAAS23562	C. albicans essent
C	148	12.8	61.0	98	25	ABX20941	Human GDP-mannose
C	149	12.8	61.0	99	24	AAAS63130	Cell death proteot
C	150	12.6	60.0	21	18	AAAT59533	Interleukin 2 rece
C	151	12.6	60.0	22	21	AAZ44872	Human apolipoprote
C	152	12.6	60.0	23	24	AAAD38675	Human CDKN1A gene
C	153	12.6	60.0	24	16	AAAT04845	PCR primer for ppr
C	154	12.6	60.0	24	24	ABO93709	Minimally cross-ly
C	155	12.6	60.0	27	16	AAO91224	Human Wnt primer-1
C	156	12.6	60.0	27	24	ABO82749	Human K+betam3 p27
C	157	12.6	60.0	27	24	ABV72205	PCR primer used to
C	158	12.6	60.0	30	16	AAO90503	Human beta-2 glyco
C	159	12.6	60.0	30	21	AAAO7855	Forward RH mapping
C	160	12.6	60.0	35	21	AAZ09570	PCR primer D used
C	161	12.6	60.0	35	21	AAZ095642	Human papillomavir
C	162	12.6	60.0	36	23	AAAT77138	Human HLA-DR alpha
C	163	12.6	60.0	37	24	AB158451	Antisense primer f
C	164	12.6	60.0	39	24	ABN61142	Human polymorphism
C	165	12.6	60.0	39	24	ABN611276	Human polymorphism
C	166	12.6	60.0	48	20	AAV65027	Human P selectin 1
C	167	12.6	60.0	51	22	AAAT27880	Human SNP oligonuc
C	168	12.6	60.0	51	22	AAAT30617	Human SNP oligonuc
C	169	12.6	60.0	51	22	AAAT76495	Human silent SNP c
C	170	12.6	60.0	60	24	ABN39177	Human spliced tran
C	171	12.6	60.0	60	24	ABN45757	Human spliced tran
C	172	12.6	60.0	60	24	ABN48071	Human spliced tran
C	173	12.6	60.0	60	24	ABN49731	Human spliced tran
C	174	12.6	60.0	65	24	ABN50876	Human spliced tran
C	175	12.6	60.0	65	24	ABZ26625	Candida essential
C	176	12.6	60.0	70	18	AAV76443	Staphylococcus aur
C	177	12.6	60.0	78	22	AAK23682	Human brain expres
C	178	12.6	60.0	78	22	AAI26908	Probe #16841 for g
C	179	12.6	60.0	78	22	AAI55707	Probe #24393 used
C	180	12.6	60.0	78	23	ABN49434	Human liver single
C	181	12.6	60.0	80	21	AAZ30402	PCR primer used to
C	182	12.6	60.0	82	19	AAV21701	Human thrombopoiet
C	183	12.6	60.0	82	19	AAV21702	Human thrombopoiet
C	184	12.6	60.0	93	16	AAAT19791	Human gene signatu
C	185	12.6	60.0	98	25	ABX33152	Human GDP-mannose
C	186	12.6	60.0	98	25	ABX33156	Synthetic oligomer
C	187	12.4	59.0	20	13	AAO31976	Synthetic oligomer
C	188	12.4	59.0	20	13	AAAS4535	Human PARP-1 anti
C	189	12.4	59.0	21	21	AAZ76335	Human diallelic ma
C	190	12.4	59.0	26	20	AAAZ5019	Cyclin-dependent K
C	191	12.4	59.0	26	20	AAAX0286	Clone th65 CDC2at
C	192	12.4	59.0	26	21	AAAS1420	Primer for A. thal
C	193	12.4	59.0	28	24	ABK13889	PCR primer TB-14 u
C	194	12.4	59.0	30	11	AAO04803	Phe-355 mutation o
C	195	12.4	59.0	30	17	AAAT34647	Primer for creatin
C	196	12.4	59.0	30	18	AAAT69804	Endo-beta-N-acetyl
C	197	12.4	59.0	30	21	AAAT75334	PCR primer Bobbigr
C	198	12.4	59.0	31	20	AAAZ33153	Trepromona pallidum
C	199	12.4	59.0	34	20	AAAX91924	Pat-6 delta 9 desa
C	200	12.4	59.0	36	20	AAZ07726	Phosphoenolpyruvat
C	201	12.4	59.0	37	24	ABL89405	Human dihydroorota
C	202	12.4	59.0	37	24	ABL89405	Porphyromonas ging
C	203	12.4	59.0	40	21	AAZ59882	C. boidini DAs ge
C	204	12.4	59.0	40	21	AAZ59884	Babesia microti an
C	205	12.4	59.0	40	21	AAZ59884	Plasmodium yoelii
C	206	12.4	59.0	40	21	AAZ59884	Primer #1 used in
C	207	12.4	59.0	40	25	AAO36827	Maize polymorphic
C	208	12.4	59.0	41	19	AAV47728	Human map-related
C	209	12.4	59.0	47	21	AAZ65975	Human silent SNP c
C	210	12.4	59.0	50	22	AAAT76865	Human silent SNP c
C	211	12.4	59.0	50	22	AAAT76867	Human silent SNP c
C	212	12.4	59.0	50	24	ABZ02961	Human leukocyte ge
C	213	12.4	59.0	51	22	AAAT76864	Human silent SNP c
C	214	12.4	59.0	51	22	AAAT76866	Human silent SNP c
C	215	12.4	59.0	51	22	AAAT76866	Human silent SNP c
C	216	12.4	59.0	51	22	AAAT76866	Human silent SNP c
C	217	12.4	59.0	60	24	ABN45490	Human spliced tran
C	218	12.4	59.0	65	24	ABN52714	Human spliced tran
C	219	12.4	59.0	66	16	AAAT19798	Human gene signatu
C	220	12.2	58.1	17	19	AAV96668	Potato citrate syn
C	221	12.2	58.1	17	21	AAAF04361	Hammerhead ribozym
C	222	12.2	58.1	17	21	AAAF04361	Hammerhead ribozym
C	223	12.2	58.1	17	21	AAAF04361	Hammerhead ribozym
C	224	12.2	58.1	21	21	AAZ73972	Human biallelic na
C	225	12.2	58.1	22	25	ABZ79335	Acetyl-Coenzyme A-
C	226	12.2	58.1	24	16	AAO67163	Primer for amplif
C	227	12.2	58.1	24	16	AAO67163	Cytomegalovirus pr

C 228	12.2	58.1	24	16	AA085703	Interonic primer fo	C 301	12	57.1	25	24	ABN13735	Human GDM/P-1 25-m
229	12.2	58.1	24	17	AA032907	Cucumber mosaic vi	C 302	12	57.1	25	24	ABN13736	Human GDM/P-1 25-m
230	12.2	58.1	24	21	AA265180	Primer amplifying	C 303	12	57.1	25	24	ABN13737	Human GDM/P-1 25-m
231	12.2	58.1	24	22	AA244337	Human PRO828 forwa	C 304	12	57.1	25	24	ABN13738	Human GDM/P-1 25-m
232	12.2	58.1	24	24	ABK28596	Human PRO828 forwa	C 305	12	57.1	25	24	ABN13739	Human GDM/P-1 25-m
233	12.2	58.1	24	25	ABX80248	Human secreted or	C 306	12	57.1	25	24	ABN13740	Human GDM/P-1 25-m
234	12.2	58.1	24	25	ABX80752	Human secreted/tra	C 307	12	57.1	25	24	ABN13746	Human GDM/P-1 25-m
235	12.2	58.1	24	25	ABX81135	Human secreted or	C 308	12	57.1	26	18	AA167064	Human GDM/P-1 25-m
236	12.2	58.1	24	25	ABX90225	Human secreted/tra	C 309	12	57.1	27	18	ABSB67778	Human GDM/P-1 25-m
237	12.2	58.1	24	25	ABX77836	Human PRO PCR prim	C 310	12	57.1	28	22	AAAD07348	Human GDM/P-1 25-m
238	12.2	58.1	24	25	ABX79432	Human secreted/tra	C 311	12	57.1	29	21	AAAD29209	Human GDM/P-1 25-m
239	12.2	58.1	24	25	ABX64071	Human PRO DNA PCR	C 312	12	57.1	29	21	AAAD29209	Human GDM/P-1 25-m
240	12.2	58.1	24	25	ABX17035	Human PRO PCR prim	C 313	12	57.1	29	21	AAAD29209	Human GDM/P-1 25-m
C 241	12.2	58.1	26	21	AAZ93073	Primer used to gen	C 314	12	57.1	29	21	AAZ34637	Human GDM/P-1 25-m
242	12.2	58.1	28	21	AAZ37277	PCR primer for SGR	C 315	12	57.1	29	22	AAAD21738	Human GDM/P-1 25-m
C 243	12.2	58.1	29	21	AAAO7746	Human lysozyme L	C 316	12	57.1	30	18	AAAO96176	Human GDM/P-1 25-m
C 244	12.2	58.1	29	21	ABO81588	Candida albicans a	C 317	12	57.1	30	16	AAAT73024	Human GDM/P-1 25-m
C 245	12.2	58.1	30	21	AAAC69971	VEGF-binding nucle	C 318	12	57.1	30	19	AAV54895	Human GDM/P-1 25-m
C 246	12.2	58.1	30	22	AAAC66783	PCR primer used to	C 319	12	57.1	30	19	AAV54895	Human GDM/P-1 25-m
247	12.2	58.1	30	24	ABX67580	Novel Helicobacter	C 320	12	57.1	30	19	AAV54895	Human GDM/P-1 25-m
248	12.2	58.1	30	24	ABD36150	Human SGR2-alpha 9	C 321	12	57.1	30	19	AAV54895	Human GDM/P-1 25-m
C 249	12.2	58.1	31	17	AAAT3322	Primer for amplify	C 322	12	57.1	30	20	AAV54895	Human GDM/P-1 25-m
C 250	12.2	58.1	31	20	AAAX80819	Plant lumaizine syn	C 323	12	57.1	30	21	AAV54895	Human GDM/P-1 25-m
C 251	12.2	58.1	33	20	AAAX06855	BCOADC subunit B1	C 324	12	57.1	30	22	AAV54895	Human GDM/P-1 25-m
C 252	12.2	58.1	33	24	ABX55297	Human leucine zipr	C 325	12	57.1	30	22	AAV54895	Human GDM/P-1 25-m
C 253	12.2	58.1	33	24	ABX55297	Human B lymphocyte	C 326	12	57.1	30	22	AAV54895	Human GDM/P-1 25-m
C 254	12.2	58.1	34	19	AAV33583	Pyrococcus horikos	C 327	12	57.1	30	24	ABX89421	Human GDM/P-1 25-m
C 255	12.2	58.1	34	22	AAH44207	Human SHC protein	C 328	12	57.1	30	24	ABX89421	Human GDM/P-1 25-m
C 256	12.2	58.1	35	22	AAH77613	Human SHC protein	C 329	12	57.1	30	24	ABX89421	Human GDM/P-1 25-m
C 257	12.2	58.1	38	17	AAAT42470	Protein kinase 35	C 330	12	57.1	31	21	AAV54895	Human GDM/P-1 25-m
C 258	12.2	58.1	39	24	ABAO3153	Oligo M2 containin	C 331	12	57.1	31	21	AAV54895	Human GDM/P-1 25-m
C 259	12.2	58.1	40	19	AAV27005	PCR primer KSE1.	C 332	12	57.1	31	22	AAV54895	Human GDM/P-1 25-m
C 260	12.2	58.1	46	16	AAQ86497	Feline immunodefec	C 333	12	57.1	31	22	AAV54895	Human GDM/P-1 25-m
C 261	12.2	58.1	47	20	AAAX52586	E2F-1 PCR primer.	C 334	12	57.1	31	22	AAV54895	Human GDM/P-1 25-m
C 262	12.2	58.1	51	22	AAH47665	Human genome biall	C 335	12	57.1	31	22	AAV54895	Human GDM/P-1 25-m
C 263	12.2	58.1	51	22	ABL49533	Nucleotide sequenc	C 336	12	57.1	31	22	AAV54895	Human GDM/P-1 25-m
C 264	12.2	58.1	51	24	ABL49533	scFv antibody and	C 337	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 265	12.2	58.1	52	22	AAAS2536	Human ovarian PCR-	C 338	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 266	12.2	58.1	53	21	AAAG94950	S. capricanis smal	C 339	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 267	12.2	58.1	53	21	AAAG94950	S. tenella small r	C 340	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 268	12.2	58.1	58	21	AAAC70040	VEGF-binding nucle	C 341	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 269	12.2	58.1	60	20	AAAT79677	VEGF-binding nucle	C 342	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 270	12.2	58.1	60	22	AAAT79677	Human LKB1 gene pr	C 343	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 271	12.2	58.1	60	22	AAAT79677	Mouse LKB1 express	C 344	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 272	12.2	58.1	60	22	AAAT79677	Human LKB1 gene pr	C 345	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 273	12.2	58.1	60	24	ABN37796	Human spliced tran	C 346	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 274	12.2	58.1	60	24	ABN49287	Human spliced tran	C 347	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 275	12.2	58.1	61	21	AAAC69863	MEK/ERK signal tra	C 348	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 276	12.2	58.1	64	22	AAAF5414	VEGF-binding nucle	C 349	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 277	12.2	58.1	64	24	ABX91350	PCR primer for gly	C 350	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 278	12.2	58.1	64	24	ABX91350	Pichia methanolica	C 351	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 279	12.2	58.1	65	21	AAAC11260	Human secreted pro	C 352	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 280	12.2	58.1	65	21	AAAC11260	CBE-tagged-Zs1g57	C 353	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 281	12.2	58.1	65	24	ABZ28531	Candida essential	C 354	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 282	12.2	58.1	65	24	ABZ28531	Candida gene relat	C 355	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 283	12.2	58.1	65	24	ABZ28531	Candida gene relat	C 356	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 284	12.2	58.1	65	24	ABZ28531	Mouse spliced tran	C 357	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 285	12.2	58.1	67	24	AAAD41830	Upper PCR primer t	C 358	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 286	12.2	58.1	84	24	ABN62226	Human cancer relat	C 359	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 287	12.2	58.1	89	22	AAH42549	Nucleotide sequenc	C 360	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 288	12.2	58.1	100	15	AAO62584	Candida albicans-s	C 361	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 289	12.2	58.1	112	22	AAAF56231	DNA binding protei	C 362	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 290	12.2	58.1	112	22	ABAF78121	BRCA1 mutation cor	C 363	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 291	12.2	58.1	17	22	ABAF78121	BRCA1 mutation cor	C 364	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 292	12.2	58.1	17	24	ABN85818	Related to Bombyx	C 365	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 293	12.2	58.1	20	22	AAH80632	Oligonucleotide hy	C 366	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 294	12.2	58.1	20	23	ABZ26010	Rat beta-casein ST	C 367	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 295	12.2	58.1	22	21	AAZ92401	Human galectin-1 o	C 368	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 296	12.2	58.1	22	21	AAZ92401	CMV gene fragmen	C 369	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 297	12.2	58.1	22	22	AAAF57263	CMV gene fragmen	C 370	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 298	12.2	58.1	22	22	AAAF57263	Nucleic acid of th	C 371	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 299	12.2	58.1	24	22	AAAF30349	Nucleic acid of th	C 372	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m
C 300	12.2	58.1	24	25	ABZ56927	Isotopic purinore	C 373	12	57.1	31	24	ABX89421	Human GDM/P-1 25-m

C 374	12	57.1	50	18	AA774745	EV152 used in cons	C 447	11.8	56.2	21	20	AAV65021	Human P selectin 1
C 375	12	57.1	50	21	AAZ43940	A. gossypii riba p	C 448	11.8	56.2	22	19	AAV67258	IFN-gamma PCR sens
C 376	12	57.1	50	24	ABZ00743	Human leukocyte ge	C 449	11.8	56.2	24	12	AAO10681	Probe for arginine
C 377	12	57.1	50	24	ABZ05089	Human leukocyte ge	C 450	11.8	56.2	24	17	AA741739	Clockwise primer f
C 378	12	57.1	50	24	ABZ05928	Human leukocyte ge	C 451	11.8	56.2	24	22	AAH37901	SNP specific primer f
C 379	12	57.1	50	24	ABZ07660	Human leukocyte ge	C 452	11.8	56.2	24	22	ABJ54213	Human CCR4 related
C 380	12	57.1	51	17	AA713495	Sept methylase 5'	C 453	11.8	56.2	25	15	AAO61498	Oligomer compriatin
C 381	12	57.1	51	22	AA559986	Canine IL-13Ralpha	C 454	11.8	56.2	25	19	AAV64592	Human native inter
C 382	12	57.1	51	22	AA76275	Human silent SNP c	C 455	11.8	56.2	25	19	AAV67060	Mouse ikaros oligo
C 383	12	57.1	51	22	AA76948	Human silent SNP c	C 456	11.8	56.2	25	19	AAV45353	Human Apob gene G
C 384	12	57.1	51	22	AA76949	Human silent SNP c	C 457	11.8	56.2	25	21	AAH07964	Human Apob gene PC
C 385	12	57.1	52	20	AA575539	RT-PCR primer for	C 458	11.8	56.2	25	21	AAH07965	Human Apob gene PC
C 386	12	57.1	52	22	AAH29538	Drosophila melanog	C 459	11.8	56.2	25	21	AAH07972	SNP specific lower
C 387	12	57.1	53	21	AAA94948	S. neurena small ri	C 460	11.8	56.2	27	22	AAH39258	Chicken fgf-4 gene
C 388	12	57.1	53	21	AAA94955	T. gondii small ri	C 461	11.8	56.2	28	22	AAH76130	Chicken fibroblast
C 389	12	57.1	60	21	AAA53674	Oligonucleotide us	C 462	11.8	56.2	28	22	AAH10169	PCR primer for amp
C 390	12	57.1	60	21	AAA53693	Oligonucleotide us	C 463	11.8	56.2	28	22	AAH87095	PCR primer for amp
C 391	12	57.1	60	21	ABN34077	Human spliced tran	C 464	11.8	56.2	28	24	ABH87567	Chicken Fgf-4 gene
C 392	12	57.1	60	24	ABN34657	Human spliced tran	C 465	11.8	56.2	28	24	ABJ41654	pHPTSI sense prim
C 393	12	57.1	60	24	ABN35926	Human spliced tran	C 466	11.8	56.2	29	14	AAQ46190	GH1P19-R3 reverse
C 394	12	57.1	60	24	ABN40968	Human spliced tran	C 467	11.8	56.2	29	19	AAV64604	Human native inter
C 395	12	57.1	60	24	ABN42010	Human spliced tran	C 468	11.8	56.2	29	21	AAH40600	Human Arp3H PCR pr
C 396	12	57.1	60	24	ABN44193	Human spliced tran	C 469	11.8	56.2	29	22	AAH82369	Chicken embryo let
C 397	12	57.1	60	24	ABN46845	Human spliced tran	C 470	11.8	56.2	30	17	AAH70701	Primer 17A-NF, 5'
C 398	12	57.1	60	24	ABN47344	Human spliced tran	C 471	11.8	56.2	30	21	AAA51328	Primer w258_ZMW14
C 399	12	57.1	60	24	ABN47723	Human spliced tran	C 472	11.8	56.2	30	21	AAA51551	Primer for Z. mays
C 400	12	57.1	60	24	ABN47723	G3 oligo (60mer) u	C 473	11.8	56.2	30	21	AAA30654	Human G protein-co
C 401	12	57.1	60	25	AAH47389	Oligonucleotide G3	C 474	11.8	56.2	30	22	AAH19630	Staphylococcus aur
C 402	12	57.1	62	21	AAA32229	Chromosome 12 olig	C 475	11.8	56.2	32	20	AAV55575	Primer for Aquif cy
C 403	12	57.1	65	21	AAZ92402	Human galectin-1 o	C 476	11.8	56.2	32	22	AAH43950	Binary vector cons
C 404	12	57.1	65	24	ABZ27573	Candida gene relat	C 477	11.8	56.2	32	22	AAH25186	PCR primer used to
C 405	12	57.1	65	24	ABZ28714	Candida gene relat	C 478	11.8	56.2	33	16	AAQ91629	Human apolipoprote
C 406	12	57.1	65	24	ABZ28834	Candida gene relat	C 479	11.8	56.2	33	21	AAA52588	Wildtype early reg
C 407	12	57.1	65	24	ABN29642	Rat spliced transc	C 480	11.8	56.2	33	21	AAA52588	Adenovirus 5 E2A r
C 408	12	57.1	65	24	ABN30444	Rat spliced transc	C 481	11.8	56.2	33	22	AAH80212	PCR primer used to
C 409	12	57.1	65	24	ABN31702	Rat spliced transc	C 482	11.8	56.2	33	22	AAH55464	PCR primer used to
C 410	12	57.1	65	24	ABN54592	Mouse spliced tran	C 483	11.8	56.2	33	22	AAH58072	Adenovirus E2A cod
C 411	12	57.1	65	24	ABN55143	Mouse spliced tran	C 484	11.8	56.2	33	22	AAH88883	Adenovirus E2A p1
C 412	12	57.1	65	24	ABN56337	Mouse spliced tran	C 485	11.8	56.2	33	24	ABH57396	PCR primer #2 for
C 413	12	57.1	78	24	ABH10528	BRCA1 exon1 mut GI	C 486	11.8	56.2	33	24	ABH86249	Transcription cont
C 414	12	57.1	78	24	ABH10542	Human BRCA1 DNA fr	C 487	11.8	56.2	33	24	ABH55125	Human Myb protein
C 415	12	57.1	84	21	AAA75363	Nucleotide fragmen	C 488	11.8	56.2	33	24	ABH05169	Human gamma glutam
C 416	12	57.1	87	25	ABX30336	Human GDP-mannose	C 489	11.8	56.2	34	22	AAH45418	PCR primer specificl
C 417	12	57.1	89	22	ABH47270	Human foetal liver	C 490	11.8	56.2	35	13	AAQ28019	VN (lys40-Pro125)
C 418	12	57.1	89	22	AAK27235	Human brain expres	C 491	11.8	56.2	35	21	AAA28204	Forward primer EQ3
C 419	12	57.1	89	22	AAK48993	Human bone marrow	C 492	11.8	56.2	36	21	AAH66175	Insert used in rep
C 420	12	57.1	89	22	AAH54730	Probe #23416 used	C 493	11.8	56.2	36	21	AAH66175	Insert used in rep
C 421	12	57.1	89	24	ABH48570	Human liver single	C 494	11.8	56.2	37	17	AAH37708	N-Acetylglucosamin
C 422	12	57.1	93	24	ABH71275	Streptococcus poly	C 495	11.8	56.2	37	17	AAH37708	Human parvovirus B
C 423	12	57.1	94	21	AAH17410	Human secreted pro	C 496	11.8	56.2	41	17	AAH42501	Primer for preCPB
C 424	12	57.1	95	21	AAH25786	Human secreted pro	C 497	11.8	56.2	41	17	AAH42501	Primer 2265 for ma
C 425	12	57.1	96	22	AAH57107	Probe #25793 used	C 498	11.8	56.2	41	19	AAV50870	Maize polymorphic
C 426	12	57.1	96	25	ABH25824	N. gonorrhoeae nuc	C 499	11.8	56.2	41	19	AAV41802	Human pancreatic c
C 427	12	57.1	97	16	AAH081929	Interferon-gamma b	C 500	11.8	56.2	41	24	ABH257759	Human immune avidi
C 428	12	57.1	97	21	AAH10062	"Mosaic" direct re	C 501	11.8	56.2	41	24	ABH257760	Human immune avidi
C 429	12	57.1	98	16	AAH081643	bEGF binding oligo	C 502	11.8	56.2	45	18	AAH77833	Neisseria meningit
C 430	12	57.1	98	16	AAH080991	HIV protease inhib	C 503	11.8	56.2	45	21	AAH65012	Oligonucleotide #2
C 431	12	57.1	98	16	AAH080968	HIV protease inhib	C 504	11.8	56.2	45	21	AAH65043	Oligonucleotide #3
C 432	12	57.1	98	16	AAH24684	Human ovarian PCR-	C 505	11.8	56.2	46	19	AAH22301	PCR primer T2R5 us
C 433	12	57.1	98	22	AAH83310	Human ovarian tumo	C 506	11.8	56.2	46	21	AAH14412	Human tissue inhib
C 434	12	57.1	99	21	AAH834573	Human secreted pro	C 507	11.8	56.2	46	21	AAH28629	Forward PCR primer
C 435	12	57.1	100	21	AAH21056	Human low adenosin	C 508	11.8	56.2	47	21	AAH267545	Human map-related
C 436	12	57.1	100	21	AAH44934	Human adenosine re	C 509	11.8	56.2	47	21	AAH00191	Human interferon-b
C 437	12	56.2	15	17	AAH6580	Human CD40 hammerh	C 510	11.8	56.2	47	25	AAH22446	Human P selectin 1
C 438	12	56.2	17	21	AAH04362	Hammerhead ribozym	C 511	11.8	56.2	48	20	AAH56025	Probe used to isol
C 439	12	56.2	17	21	AAH04362	Hammerhead ribozym	C 512	11.8	56.2	50	20	AAH52319	Human Apob gene A-
C 440	12	56.2	18	15	AAH79288	Human c-rafc-1 onco	C 513	11.8	56.2	50	21	AAH07967	Human Apob gene G-
C 441	12	56.2	20	19	AAH79556	Mass spectrometric	C 514	11.8	56.2	50	21	AAH07968	Human oligonucleot
C 442	12	56.2	20	20	AAH24040	Human RAD1 gene pr	C 515	11.8	56.2	50	21	AAH28206	Human oligonucleot
C 443	12	56.2	20	20	AAH21358	Recombinant HIV-1	C 516	11.8	56.2	50	21	AAH28207	Human PRO221 DNA p
C 444	12	56.2	20	22	AAH65510	Zea mays root cap	C 517	11.8	56.2	50	21	AAH72477	Human PRO polyptic
C 445	12	56.2	21	19	AAH55542	Helicobacter pylor	C 518	11.8	56.2	50	22	AAH72477	Human PRO polyptic
C 446	12	56.2	21	19	AAH50498	Yeast detection pr	C 519	11.8	56.2	50	22	AAH72477	Human PRO221 Hybri

C 520	11.8	56.2	50	24	ABZ00645	Human leukocyte ge	593	11.6	55.2	31	16	AAO93681	Human stromelysin
C 521	11.8	56.2	50	24	ABZ08100	Human leukocyte ge	594	11.6	55.2	31	16	AAQ93682	Human stromelysin
C 522	11.8	56.2	50	25	ACAS4872	Novel secreted and	595	11.6	55.2	31	16	AAQ93791	Human stromelysin
C 523	11.8	56.2	50	25	ACAS5837	Probe #14 used to	596	11.6	55.2	31	16	AAQ93792	Human stromelysin
C 524	11.8	56.2	50	25	ACAS6064	Human secreted/tra	597	11.6	55.2	31	16	AAQ93793	Human stromelysin
C 525	11.8	56.2	50	25	ACA05402	Human secreted pro	598	11.6	55.2	31	16	AAQ93794	Human stromelysin
C 526	11.8	56.2	50	25	ABX96081	Human secreted/tra	599	11.6	55.2	31	17	AAK63698	Human stromelysin
C 527	11.8	56.2	50	25	ABX71512	Human secreted/tra	600	11.6	55.2	31	17	AAK63699	Human stromelysin
C 528	11.8	56.2	51	19	AAV07047	Truncated barbouri	601	11.6	55.2	31	17	AAK63700	Human stromelysin
C 529	11.8	56.2	51	19	AAV07042	Truncated barbouri	602	11.6	55.2	31	17	AAK63701	Human stromelysin
C 530	11.8	56.2	51	19	AAV06924	Truncated barbouri	603	11.6	55.2	31	17	AAK63587	Human stromelysin
C 531	11.8	56.2	51	22	AAI32091	Human SNP oligonuc	604	11.6	55.2	31	17	AAK63588	Human stromelysin
C 532	11.8	56.2	56	25	ABZ78486	Tumour suppression	605	11.6	55.2	31	17	AAK63589	Human stromelysin
C 533	11.8	56.2	56	25	ABZ09033	Human oligonucleot	606	11.6	55.2	32	15	AAQ68560	Primer for amplify
C 534	11.8	56.2	60	21	AAAI5063	5' PCR primer for	607	11.6	55.2	32	19	AAV28283	Nuclear location s
C 535	11.8	56.2	60	21	AAAD00107	Human interferon-b	608	11.6	55.2	33	22	AAH44347	Human DNA polymera
C 536	11.8	56.2	60	24	ABN33107	Human spliced tran	609	11.6	55.2	33	22	AAH98246	C neofornans strai
C 537	11.8	56.2	60	24	ABN43173	Human spliced tran	610	11.6	55.2	33	24	ABO83920	Mouse polycomb gen
C 538	11.8	56.2	60	24	ABN45708	Human spliced tran	611	11.6	55.2	33	24	ABD22242	Mouse polycomb gen
C 539	11.8	56.2	60	24	ABN45798	Human spliced tran	612	11.6	55.2	36	21	AAK32189	MTA 5' P13L flanki
C 540	11.8	56.2	62	21	AAZ96839	S. cerevisiae gene	613	11.6	55.2	36	21	AAA32202	First probe subunit
C 541	11.8	56.2	64	16	AAQ87138	Primer EV29 binds	614	11.6	55.2	36	21	AAA32219	Upstream target su
C 542	11.8	56.2	64	17	AAI32719	Oligo EV29 for cre	615	11.6	55.2	39	21	AAV75930	Capture probe subu
C 543	11.8	56.2	64	18	AAI60980	5'-end of alpha w	616	11.6	55.2	40	24	ABA51672	PCR primer used to
C 544	11.8	56.2	64	18	AAI73267	Upstream primer EV	617	11.6	55.2	41	22	AAH44349	Staphylococcus aur
C 545	11.8	56.2	64	19	AAV58337	Primer EV29 for ha	618	11.6	55.2	41	22	AAH43922	Human DNA polymera
C 546	11.8	56.2	64	22	AAI681475	Human alpha globin	619	11.6	55.2	41	24	ABQ83922	Mouse polycomb gen
C 547	11.8	56.2	65	21	AAAS58805	Primer for the bet	620	11.6	55.2	42	22	AAI68554	Mouse polycomb gen
C 548	11.8	56.2	65	24	ABBS3154	Human galactosyltr	621	11.6	55.2	42	22	AAI68554	Human cytochrome p
C 549	11.8	56.2	65	24	AAAD39790	ZC2564 PCR primer	622	11.6	55.2	42	25	ABZ24753	PCR primer 24 used
C 550	11.8	56.2	65	24	ABN51792	Mouse spliced tran	623	11.6	55.2	43	24	ABZ27765	Human P-cadherin r
C 551	11.8	56.2	65	24	ABN56804	Mouse spliced tran	624	11.6	55.2	44	22	ABD12978	Candida essential
C 552	11.8	56.2	75	21	AAI614517	Human secreted pro	625	11.6	55.2	45	10	AAAN91228	Human DSP-13 cDNA
C 553	11.8	56.2	90	21	ABL78296	Human ovarian canc	626	11.6	55.2	46	16	AAQ92024	Linker sequence fo
C 554	11.8	56.2	91	21	AAI619655	Human secreted pro	627	11.6	55.2	46	20	AAZ23092	polynucleotide use
C 555	11.8	56.2	92	24	ABX66053	Helicobacter pylor	628	11.6	55.2	47	21	AAZ67366	A. thaliana gene a
C 556	11.8	56.2	93	25	ABZ19317	Group III cDNA can	629	11.6	55.2	48	20	AAZ96657	Human map-related
C 557	11.8	56.2	98	21	AAZ28944	Human secreted pro	630	11.6	55.2	49	20	AAZ23769	T cell antigen rec
C 558	11.8	56.2	98	21	AAZ42502	Human 5' EST isola	631	11.6	55.2	50	22	AAI33800	Vector pAS1.0 PCR
C 559	11.8	56.2	100	22	AAI63612	Saccharomyces cere	632	11.6	55.2	50	22	AAI75663	Human SNP oligonuc
C 560	11.6	55.2	20	24	ABN79757	Human Fas target c	633	11.6	55.2	50	22	ABZ01004	Human silent SNP c
C 561	11.6	55.2	22	22	AAI64575	PCR primer used fo	634	11.6	55.2	50	24	ABZ01075	Human leukocyte ge
C 562	11.6	55.2	22	24	ABT06693	Nucleic acid detec	635	11.6	55.2	50	24	ABZ01076	Human leukocyte ge
C 563	11.6	55.2	23	24	ABX05519	PEPT B-3' adapter	636	11.6	55.2	50	24	ABZ02485	Human leukocyte ge
C 564	11.6	55.2	23	24	ABQ80686	Murine p85 PCR pri	637	11.6	55.2	50	24	ABZ07859	Human leukocyte ge
C 565	11.6	55.2	24	22	AAH25679	PCR primer for hum	638	11.6	55.2	51	22	AAI27324	Human SNP oligonuc
C 566	11.6	55.2	24	24	ABQ93709	Minimally cross-hy	639	11.6	55.2	51	22	AAI75662	Human silent SNP c
C 567	11.6	55.2	24	24	ABL583235	PCR primer C-XBAI	640	11.6	55.2	51	22	AAH39576	Human SNP flankin
C 568	11.6	55.2	24	24	ABA04808	Ligase coenzyme A	641	11.6	55.2	51	22	AAH39676	Human SNP flankin
C 569	11.6	55.2	25	19	AAV62611	LO-CD2A chimeric a	642	11.6	55.2	52	16	AAI19845	Human gene signatu
C 570	11.6	55.2	25	19	AAV22867	MHC heavy chain ve	643	11.6	55.2	53	21	AAV94949	S. muris small rib
C 571	11.6	55.2	25	20	AAZ10136	PCR primer used to	644	11.6	55.2	56	22	AAI64190	H1rudin/oprf fusio
C 572	11.6	55.2	25	22	AAI69668	Hepatitis B virus	645	11.6	55.2	59	16	AAI22863	Human gene signatu
C 573	11.6	55.2	25	22	AAH39675	SNP specific SNPE	646	11.6	55.2	60	20	AAH66432	Human single nucle
C 574	11.6	55.2	26	19	AAV62662	Humanised antibody	647	11.6	55.2	60	24	ABN34741	Human spliced tran
C 575	11.6	55.2	26	19	AAV22895	Humanised LO-CD2A	648	11.6	55.2	60	24	ABN36820	Human spliced tran
C 576	11.6	55.2	26	20	AAZ10195	PCR primer used to	649	11.6	55.2	60	24	ABN39541	Human spliced tran
C 577	11.6	55.2	27	24	ABK86266	Megaspheara cerevi	650	11.6	55.2	60	24	ABN40667	Human spliced tran
C 578	11.6	55.2	27	24	ABL58545	Human PMP1 gene hy	651	11.6	55.2	60	24	ABN41514	Human spliced tran
C 579	11.6	55.2	27	25	ABLS56525	Mouse HPRT RT-PCR	652	11.6	55.2	60	24	ABN44338	Human spliced tran
C 580	11.6	55.2	28	22	AAI24577	PCR primer used fo	653	11.6	55.2	60	24	ABN48166	Human spliced tran
C 581	11.6	55.2	28	24	ABD43093	T. pllicata TPDIR9	654	11.6	55.2	64	24	ABN48980	Human spliced tran
C 582	11.6	55.2	28	24	ABT06695	Nucleic acid detec	655	11.6	55.2	64	13	AAQ25731	Human spliced tran
C 583	11.6	55.2	29	18	AAI964821	Primer OTG4169 for	656	11.6	55.2	64	22	AAI55414	N-terminal extrace
C 584	11.6	55.2	30	14	AAQ48421	Antisense primer f	657	11.6	55.2	64	22	ABK91350	PCR primer for gly
C 585	11.6	55.2	30	15	AAQ73169	Antisense primer f	658	11.6	55.2	64	24	AAK98884	Pichia methanolica
C 586	11.6	55.2	30	16	AAI73942	Primer 75 for huma	659	11.6	55.2	65	21	AAA14522	Pichia methanolica
C 587	11.6	55.2	30	16	AAI707629	Antisense primer 7	660	11.6	55.2	65	22	AAI18424	PCR primer used to
C 588	11.6	55.2	30	16	AAI700657	Antisense primer 7	661	11.6	55.2	65	22	ABZ26436	Asbbya gossypii ge
C 589	11.6	55.2	30	19	AAV34557	Homo sapiens RNA 3	662	11.6	55.2	65	24	ABZ28550	Candida gene relat
C 590	11.6	55.2	30	20	AAK87928	Human PCIP PCR pri	663	11.6	55.2	65	24	ABZ28778	Candida gene relat
C 591	11.6	55.2	30	20	AAK21759	AOB promoter BCB	664	11.6	55.2	65	24	ABZ28935	Candida gene relat
C 592	11.6	55.2	31	16	AAQ93680	Human stromelysin	665	11.6	55.2	65	24	ABN28846	Rat spliced transc



666	11.6	55.2	65	24	ABN30342	Rat spliced transc	c 739	11.4	54.3	20	21	AAA41115	Human TNFalpha ant
667	11.6	55.2	65	24	ABN53729	Mouse spliced tran	740	11.4	54.3	20	21	AAZ89825	PCR primer for car
668	11.6	55.2	65	24	ABN55272	Mouse spliced tran	741	11.4	54.3	20	21	AAZ88038	Human umbilical ve
669	11.6	55.2	66	20	AAH85630	Human single nucle	742	11.4	54.3	21	21	AAA97254	PRRV attenuated v
670	11.6	55.2	68	24	ABJ36201	C. elegans connect	743	11.4	54.3	21	21	ABK27416	Human papillomavir
671	11.6	55.2	69	24	ABJ98840	Oligonucleotide MP	744	11.4	54.3	21	25	ABZ23539	PCR primer used to
672	11.6	55.2	72	19	AAV62650	Humanised antibody	745	11.4	54.3	21	25	ABZ23555	PCR primer used to
673	11.6	55.2	72	20	AAZ32795	Reshaped F19 light	746	11.4	54.3	22	19	AAV07499	Leistad virus pri
674	11.6	55.2	72	20	AAZ32800	Reshaped F19 light	747	11.4	54.3	23	20	AAZ30818	STAT-3 specific ol
675	11.6	55.2	72	20	AAZ10183	Oligonucleotide 12	748	11.4	54.3	23	22	AAZ33446	Reverse PCR primer
676	11.6	55.2	72	21	AACT1559	Human secreted pro	749	11.4	54.3	24	24	ABJ54091	Human nucleotide e
677	11.6	55.2	72	21	AACT1354	Human secreted pro	750	11.4	54.3	24	24	ABJ54091	Human zinc finger
678	11.6	55.2	74	20	AAV24800	D. pteronyssinus D	751	11.4	54.3	24	25	AAJ53759	Single sequence 1e
679	11.6	55.2	75	20	AAK37817	Primer 2. Synthet	752	11.4	54.3	25	16	AAO81978	Human soluble lamp
680	11.6	55.2	75	22	AAK19763	Human brain expres	753	11.4	54.3	25	19	AAV09946	Human CDP-diacylg
681	11.6	55.2	75	23	ABJ54574	Human liver single	754	11.4	54.3	25	24	ABK69046	Human alpha relate
682	11.6	55.2	75	24	ABJ52063	Human genome-deriv	755	11.4	54.3	25	25	ABK95049	Human oligonucleot
683	11.6	55.2	76	19	AAV21712	Thrombopoietin exp	756	11.4	54.3	25	25	ABK10925	Human CDP-diacylg
684	11.6	55.2	77	7	AAV60749	Sequence encoding	757	11.4	54.3	26	14	AAQ40023	PCR primer for OTC
685	11.6	55.2	77	7	AAV60750	Sequence encoding	758	11.4	54.3	26	15	AAQ53980	Human OTC gene pri
686	11.6	55.2	77	18	AAK11545	Human biallelic po	759	11.4	54.3	26	15	AAV45540	Helicobacter pylor
687	11.6	55.2	78	19	AAV79205	Staphylococcus aur	760	11.4	54.3	27	15	AAQ61018	COL2A1 3'-primer (
688	11.6	55.2	78	25	AAV52080	Anti-ovarian cance	761	11.4	54.3	27	16	AAQ91225	Human Wnt primer-2
689	11.6	55.2	79	22	ABA48892	Human breast cell	762	11.4	54.3	27	17	AAV22010	Primer detects mar
690	11.6	55.2	79	22	ABA49393	Human breast cell	763	11.4	54.3	27	17	AAV22010	Primer detects mar
691	11.6	55.2	79	22	ABA67303	Human foetal liver	764	11.4	54.3	27	21	AAA61722	Human serine prote
692	11.6	55.2	79	22	ABA33875	Probe #12341 for g	765	11.4	54.3	27	22	AAH75625	Aminoglycoside 3'-
693	11.6	55.2	79	22	ABA34397	Probe #12863 for g	766	11.4	54.3	27	23	ABJ53329	Artificial secreto
694	11.6	55.2	79	22	AAK15740	Human brain expres	767	11.4	54.3	27	23	ABJ53329	Primer STAS for h
695	11.6	55.2	79	22	AAK10965	Human bone marrow	768	11.4	54.3	29	17	AAI33710	Primer FAT2 used
696	11.6	55.2	79	22	AAK14177	Human bone marrow	769	11.4	54.3	29	22	AAH38245	SNP specific upper
697	11.6	55.2	79	22	AAI21735	Probe #11668 for g	770	11.4	54.3	29	22	AAH38245	Human TAC1-Fc fusi
698	11.6	55.2	79	22	AAI22235	Probe #12158 for g	771	11.4	54.3	29	25	AAJ53763	Human TAC1-Fc fusi
699	11.6	55.2	79	22	AAI47020	Probe #15706 used	772	11.4	54.3	30	18	AAV58275	M3mpla PCR primer
700	11.6	55.2	79	22	AAI47520	Probe #16206 used	773	11.4	54.3	30	21	ABJ41542	Nucleotide sequenc
701	11.6	55.2	79	22	AAI07420	Probe #7411 used t	774	11.4	54.3	30	22	AAJ50691	Forward PCR primer
702	11.6	55.2	79	23	AAI07923	Probe #7914 used t	775	11.4	54.3	30	22	AAJ50691	Forward PCR primer
703	11.6	55.2	79	23	ABJ40548	Human liver single	776	11.4	54.3	30	22	AAJ50691	Forward PCR primer
704	11.6	55.2	79	24	ABJ41068	Human liver single	777	11.4	54.3	30	24	ABO4680	Paddy rice melotic
705	11.6	55.2	79	24	ABJ41932	Human genome-deriv	778	11.4	54.3	31	19	AAV03561	Probe b104 for re
706	11.6	55.2	79	24	ABJ51542	Human genome-deriv	779	11.4	54.3	31	20	AAJ17797	Wheat oxalate oxid
707	11.6	55.2	82	19	AAV21714	Thrombopoietin exp	780	11.4	54.3	31	20	AAK02833	Wheat oxalate oxid
708	11.6	55.2	82	22	ABA40731	Human brain expres	781	11.4	54.3	32	16	AAQ83193	Primer used to cre
709	11.6	55.2	82	22	AAK24845	Human brain expres	782	11.4	54.3	33	22	AAH75925	Human ATPase 30 c
710	11.6	55.2	82	22	AAK24845	Human bone marrow	783	11.4	54.3	33	22	AAJ51737	Mutant human facto
711	11.6	55.2	82	24	ABJ52083	Human genome-deriv	784	11.4	54.3	33	24	AAJ51737	Heparin binding pr
712	11.6	55.2	86	21	AAK52889	Arabidopsis thalia	785	11.4	54.3	33	24	ABJ56688	Fragile intelligen
713	11.6	55.2	90	22	AAK52889	Tetracycline promo	786	11.4	54.3	33	24	ABJ56688	Human phosphatid
714	11.6	55.2	91	24	ABJ52083	Tumour suppression	787	11.4	54.3	33	24	ABJ56688	Human serine thre
715	11.6	55.2	95	21	AAK26011	Human secreted pro	788	11.4	54.3	34	20	AAJ51970	Porphyromonas ging
716	11.6	55.2	97	16	AAO80978	HIV protease inh	789	11.4	54.3	34	25	ABJ73365	Endothelially expr
717	11.6	55.2	97	16	AAO80978	HIV protease inh	790	11.4	54.3	35	24	ABK47845	Borrelia OspA-B31/
718	11.6	55.2	97	16	AAO80978	HIV protease inh	791	11.4	54.3	36	16	AAO80978	Alur gene PCR pri
719	11.6	55.2	97	21	AAK21054	Human low adenosi	792	11.4	54.3	36	19	AAV59183	Human bak BH2 doma
720	11.6	55.2	98	16	AAQ01895	Interferon-gamma b	793	11.4	54.3	36	19	AAV59183	Cryptococcus nodae
721	11.6	55.2	98	16	AAQ01895	HIV protease inh	794	11.4	54.3	37	19	AAV62623	LO-CD2a chimeric a
722	11.6	55.2	98	16	AAQ01895	HIV protease inh	795	11.4	54.3	37	20	AAZ10148	PCR primer used to
723	11.6	55.2	98	24	ABJ52083	Tumour suppression	796	11.4	54.3	38	24	ABK47847	Borrelia OspA-B31/
724	11.6	55.2	99	25	ABK06081	S. pneumoniae type	797	11.4	54.3	38	24	ABK16706	Apal restriction s
725	11.6	55.2	100	21	AAK13251	Human secreted pro	798	11.4	54.3	38	24	ABK16706	Apal restriction s
726	11.6	55.2	100	21	AAK13251	Oligonucleotide SE	799	11.4	54.3	39	16	AAK16707	CryI toxin PCR pri
727	11.4	54.3	13	23	ABJ52083	Oligonucleotide SE	800	11.4	54.3	39	16	AAK16707	CryI toxin PCR pri
728	11.4	54.3	13	23	ABJ52083	Oligonucleotide SE	801	11.4	54.3	39	16	AAK16707	CryI toxin PCR pri
729	11.4	54.3	15	17	AAK65579	Human CD40 hammet	802	11.4	54.3	39	19	AAV26116	Bt toxin PCR prime
730	11.4	54.3	17	13	AAQ23301	Probe to alphaW-P	803	11.4	54.3	39	21	AAZ58029	SIV NA gene PCR pr
731	11.4	54.3	18	20	AAK21745	Competitor oligo A	804	11.4	54.3	39	21	AAZ58029	Swine influenza vi
732	11.4	54.3	18	22	AAK26521	Human SRC-3 antise	805	11.4	54.3	39	22	AAH23591	E coli ATP synthas
733	11.4	54.3	20	20	AAK97434	Primer used to amp	806	11.4	54.3	41	22	AAH78578	Upstream primer MP
734	11.4	54.3	20	20	AAK97434	Reverse primer for	807	11.4	54.3	41	22	AAK97434	Mutant human facto
735	11.4	54.3	20	20	AAK97434	Reverse primer for	808	11.4	54.3	41	22	AAK97434	Human GHRH 9.13 pr
736	11.4	54.3	20	20	AAK97434	Reverse primer for	809	11.4	54.3	42	22	AAH45890	C primum Cols/60 p
737	11.4	54.3	20	21	AAK86113	Human rchd024 gene	810	11.4	54.3	42	22	AAH45890	Mouse MHC S1YK enc
738	11.4	54.3	20	21	AAK86113	Human TNFalpha ant	811	11.4	54.3	43	24	ABJ27006	Candida essential

C 812	11.4	54.3	44	16	AAT04749	PCR primer, EPS42K	C 885	11.4	54.3	64	21	AACT1152	Human secreted pro
C 813	11.4	54.3	45	20	AAZ31029	PCR primer #3 used	C 886	11.4	54.3	65	24	ABZ26239	Candida essential
C 814	11.4	54.3	45	22	AAFS4768	PCR primer used to	C 887	11.4	54.3	65	24	ABZ28505	Candida gene relat
C 815	11.4	54.3	45	24	ABO81581	Luciferase gene mu	C 888	11.4	54.3	65	24	ABZ29627	Candida gene relat
C 816	11.4	54.3	45	24	ABO81582	Luciferase gene mu	C 889	11.4	54.3	65	24	ABN31044	Rat spliced trans
C 817	11.4	54.3	47	21	AAZ92750	Escherichia coli a	C 890	11.4	54.3	65	24	ABN54270	Mouse spliced tran
C 818	11.4	54.3	47	21	ABL54032	Aldehyde dehydroge	C 891	11.4	54.3	65	24	ABN55263	Mouse spliced tran
C 819	11.4	54.3	49	19	ABV64234	Plasmid pGL2-SMA2P	C 892	11.4	54.3	66	16	AAT04742	PCR primer, P1B, u
C 820	11.4	54.3	49	25	ABZ25329	PCR primer MYK150,	C 893	11.4	54.3	67	24	AAF88767	Almond HMUS PCR pr
C 821	11.4	54.3	50	20	AAZ34323	Human PRO298 hybr	C 894	11.4	54.3	67	15	AAQ63670	TNF-alpha ribozyme
C 822	11.4	54.3	50	21	AACT8900	Human PRO298 hybr	C 895	11.4	54.3	67	16	AAT24754	Human gene signatu
C 823	11.4	54.3	50	21	AAA28194	Target molecule us	C 896	11.4	54.3	67	18	AAAT45405	Specific ribozyme
C 824	11.4	54.3	50	21	AAA28197	Detection probe us	C 897	11.4	54.3	67	20	AAK05876	Interleukin 2 ribo
C 825	11.4	54.3	50	22	AAI77541	Human silent SNP c	C 898	11.4	54.3	68	25	ABZ79194	Tumour suppression
C 826	11.4	54.3	50	22	ABZ00506	Human leukocyte ge	C 899	11.4	54.3	68	25	ABZ09741	Human oligonucleot
C 827	11.4	54.3	50	24	ABZ00962	Human leukocyte ge	C 900	11.4	54.3	69	17	AAI34308	Human CSBPORI fo
C 828	11.4	54.3	50	24	ABZ02058	Human leukocyte ge	C 901	11.4	54.3	70	15	AAQ19273	Primer B850 to amp
C 829	11.4	54.3	50	24	ABZ02257	Human leukocyte ge	C 902	11.4	54.3	70	25	ABZ78951	Tumour suppression
C 830	11.4	54.3	50	24	ABZ03782	Human leukocyte ge	C 903	11.4	54.3	70	25	ABZ09498	Human oligonucleot
C 831	11.4	54.3	50	24	ABZ03923	Human leukocyte ge	C 904	11.4	54.3	71	24	ABL57259	T4 ipIII gene tran
C 832	11.4	54.3	50	24	ABZ04069	Human leukocyte ge	C 905	11.4	54.3	71	16	AAQ76253	Protease (I-247)/CK
C 833	11.4	54.3	50	24	ABZ04291	Human leukocyte ge	C 906	11.4	54.3	74	19	AAV69222	Wild type coding s
C 834	11.4	54.3	50	24	ABZ04480	Human leukocyte ge	C 907	11.4	54.3	75	19	AAV63108	Human cancer relat
C 835	11.4	54.3	50	24	ABZ05699	Human leukocyte ge	C 908	11.4	54.3	81	14	AAQ49564	Beet Cyst Nematode
C 836	11.4	54.3	50	24	AAI41463	MSMAP-5'-T7 linker	C 909	11.4	54.3	81	16	AAT06225	HIV-1 reverse tran
C 837	11.4	54.3	50	25	ABX92695	Human PRO DNA prob	C 910	11.4	54.3	85	22	AAK60150	Human immune/haema
C 838	11.4	54.3	50	25	ABZ81170	Toxicologically re	C 911	11.4	54.3	85	24	ABL75879	Corn tassell-derive
C 839	11.4	54.3	51	22	AAI27032	Human SNP oligonuc	C 912	11.4	54.3	86	19	AAV34146	Upstream primer fo
C 840	11.4	54.3	51	22	AAI32187	Human SNP oligonuc	C 913	11.4	54.3	86	19	AAV34146	Upstream primer fo
C 841	11.4	54.3	51	22	AAI73406	Human silent SNP c	C 914	11.4	54.3	86	19	AAV34278	Upstream primer fo
C 842	11.4	54.3	51	22	AAI73407	Human silent SNP c	C 915	11.4	54.3	86	19	AAV69603	Upstream primer fo
C 843	11.4	54.3	51	22	AAI75979	Human silent SNP c	C 916	11.4	54.3	86	20	AAZ32073	Gamma activation s
C 844	11.4	54.3	51	22	AAI76855	Human silent SNP c	C 917	11.4	54.3	86	20	AAZ19852	SV40 early promote
C 845	11.4	54.3	51	22	AAI77358	Human silent SNP c	C 918	11.4	54.3	86	20	AAZ24803	Upstream primer fo
C 846	11.4	54.3	51	22	AAI77359	Human silent SNP c	C 919	11.4	54.3	86	20	AAZ09776	Synthetic GAS-cont
C 847	11.4	54.3	51	22	AAI78103	Human silent SNP c	C 920	11.4	54.3	86	20	AAZ10678	PCR primer used to
C 848	11.4	54.3	51	23	ABL00202	Human silent nonco	C 921	11.4	54.3	86	20	AAZ00402	Human GAS promoter
C 849	11.4	54.3	52	12	AAQ10819	Mutated section of	C 922	11.4	54.3	86	20	AAZ00794	SV40 early promote
C 850	11.4	54.3	52	14	AAQ38444	pTPO(M1)-BS mutat	C 923	11.4	54.3	86	20	AAZ06211	Upstream primer fo
C 851	11.4	54.3	52	14	AAQ40070	Human TPO gene seq	C 924	11.4	54.3	86	20	AAV39708	Upstream primer fo
C 852	11.4	54.3	52	20	AAZ24338	Oligonucleotide 01	C 925	11.4	54.3	86	20	AAV39003	Upstream primer fo
C 853	11.4	54.3	52	24	AAI41462	MSMAP-5'-T7 linker	C 926	11.4	54.3	86	20	AAZ8669	Nucleotide sequenc
C 854	11.4	54.3	54	18	AAT98091	N-terminal primer	C 927	11.4	54.3	86	20	AAZ44925	Upstream primer fo
C 855	11.4	54.3	54	20	AAI19882	ED7-HIV p17/p24 ge	C 928	11.4	54.3	86	20	AAZ35893	PCR primer used to
C 856	11.4	54.3	54	20	AAI19526	ED7-HIV p17/p24 ge	C 929	11.4	54.3	86	20	AAZ37361	Human GAS-containi
C 857	11.4	54.3	55	21	AACT1245	Human secreted pro	C 930	11.4	54.3	86	20	AAZ37443	Synthetic GAS-cont
C 858	11.4	54.3	57	16	AAT05761	Thermophilic stran	C 931	11.4	54.3	86	20	AAZ27303	Upstream primer fo
C 859	11.4	54.3	57	22	AAD03427	MSV GC-rich elemen	C 932	11.4	54.3	86	20	AAZ51693	5' PCR primer used
C 860	11.4	54.3	57	24	ABL57260	T4 gene ipIII tran	C 933	11.4	54.3	86	20	AAZ30175	Upstream primer fo
C 861	11.4	54.3	57	24	ABL57261	Staphylococcus aur	C 934	11.4	54.3	86	20	AAZ22203	Upstream primer fo
C 862	11.4	54.3	58	18	AAV76131	Human secreted pro	C 935	11.4	54.3	86	20	AAZ22103	Upstream primer fo
C 863	11.4	54.3	59	21	AACT29473	Human secreted pro	C 936	11.4	54.3	86	20	AAZ30309	5' PCR primer used
C 864	11.4	54.3	60	24	ABN32567	Human spliced tran	C 937	11.4	54.3	86	20	AAZ20404	Upstream primer fo
C 865	11.4	54.3	60	24	ABN34745	Human spliced tran	C 938	11.4	54.3	86	20	AAZ16170	SV40 early promote
C 866	11.4	54.3	60	24	ABN37978	Human spliced tran	C 939	11.4	54.3	86	20	AAZ04303	Upstream primer fo
C 867	11.4	54.3	60	24	ABN38082	Human spliced tran	C 940	11.4	54.3	86	20	AAZ00603	Upstream primer fo
C 868	11.4	54.3	60	24	ABN38346	Human spliced tran	C 941	11.4	54.3	86	20	AAV08847	Primer for DNA enc
C 869	11.4	54.3	60	24	ABN39207	Human spliced tran	C 942	11.4	54.3	86	20	AAV84403	Upstream primer fo
C 870	11.4	54.3	60	24	ABN42543	Human spliced tran	C 943	11.4	54.3	86	21	AAD02079	SV40 promoter sequ
C 871	11.4	54.3	60	24	ABN43967	Human spliced tran	C 944	11.4	54.3	86	21	AAD02231	SV40 promoter sequ
C 872	11.4	54.3	60	24	ABN44010	Human spliced tran	C 945	11.4	54.3	86	21	AAZ22033	Upstream PCR prime
C 873	11.4	54.3	60	24	ABN44587	Human spliced tran	C 946	11.4	54.3	86	21	AAZ22308	Upstream primer fo
C 874	11.4	54.3	60	24	ABN46719	Human spliced tran	C 947	11.4	54.3	86	21	AAZ22365	Upstream primer fo
C 875	11.4	54.3	60	24	ABN49566	Human spliced tran	C 948	11.4	54.3	86	21	AAZ98765	Upstream primer fo
C 876	11.4	54.3	60	24	ABN50295	Human spliced tran	C 949	11.4	54.3	86	21	AAZ98765	Upstream primer fo
C 877	11.4	54.3	60	24	ABN58991	Human spliced tran	C 950	11.4	54.3	86	21	AAZ989810	Upstream primer fo
C 878	11.4	54.3	60	24	ABN59113	Human spliced tran	C 951	11.4	54.3	86	21	AAZ16507	Upstream primer fo
C 879	11.4	54.3	60	24	ABN59320	Human spliced tran	C 952	11.4	54.3	86	21	AAZ18426	Upstream PCR prime
C 880	11.4	54.3	61	19	AAV07498	Leiyedad virus prt	C 953	11.4	54.3	86	21	AAZ66217	Upstream primer fo
C 881	11.4	54.3	61	19	AAZ97255	PRRSV attenuated v	C 954	11.4	54.3	86	21	AAZ66402	GAS reporter const
C 882	11.4	54.3	61	24	AAZ24033	PRRSV recombinant	C 955	11.4	54.3	86	21	AAZ67623	Upstream primer fo
C 883	11.4	54.3	61	25	ABZ23556	PCR primer used to	C 956	11.4	54.3	86	21	AAZ68073	Upstream primer fo
C 884	11.4	54.3	63	21	AAZ030615	Human secreted pro	C 957	11.4	54.3	86	21	AAZ081702	GAS reporter const

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c 958 11.4 54.3 86 21 AAC93302 Upstream primer fo
c 959 11.4 54.3 86 21 AAC93356 Upstream primer fo
c 960 11.4 54.3 86 21 AAC93414 Upstream primer fo
c 961 11.4 54.3 86 21 AAC93471 Upstream primer fo
c 962 11.4 54.3 86 21 AAC95454 Upstream primer fo
c 963 11.4 54.3 86 21 AAC95513 Upstream primer fo
c 964 11.4 54.3 86 21 AAC96892 SV40 promoter upst
c 965 11.4 54.3 86 21 AAA98975 SV40 early promote
c 966 11.4 54.3 86 21 AAA98984 SV40 early promote
c 967 11.4 54.3 86 21 AAA98993 SV40 early promote
c 968 11.4 54.3 86 21 AAC98982 GAS reporter const
c 969 11.4 54.3 86 21 AAC99041 GAS reporter const
c 970 11.4 54.3 86 21 AAC99100 GAS reporter const
c 971 11.4 54.3 86 21 AAC99269 SV40 promoter upst
c 972 11.4 54.3 86 21 AAC99327 SV40 promoter upst
c 973 11.4 54.3 86 21 AAC99384 SV40 promoter upst
c 974 11.4 54.3 86 21 AAC99499 Upstream primer fo
c 975 11.4 54.3 86 21 AAC99616 Upstream primer fo
c 976 11.4 54.3 86 21 AAC99671 SV40 promoter upst
c 977 11.4 54.3 86 21 AAC93402 GAS reporter const
c 978 11.4 54.3 86 21 AAC74215 Upstream primer fo
c 979 11.4 54.3 86 21 AAC74272 Upstream primer fo
c 980 11.4 54.3 86 21 AAC74329 Upstream primer fo
c 981 11.4 54.3 86 21 AAC74388 Upstream primer fo
c 982 11.4 54.3 86 21 AAC78450 Upstream primer fo
c 983 11.4 54.3 86 21 AAC78989 Upstream primer fo
c 984 11.4 54.3 86 21 AAC79673 Upstream primer fo
c 985 11.4 54.3 86 21 AAC79732 Upstream primer fo
c 986 11.4 54.3 86 21 AAC79791 Upstream primer fo
c 987 11.4 54.3 86 21 AAC80523 Upstream primer fo
c 988 11.4 54.3 86 21 AAC81020 Upstream primer fo
c 989 11.4 54.3 86 21 AAC81078 Upstream primer fo
c 990 11.4 54.3 86 21 AAA95093 Upstream primer fo
c 991 11.4 54.3 86 21 AAC99207 Upstream primer fo
c 992 11.4 54.3 86 21 AAC99441 Upstream primer fo
c 993 11.4 54.3 86 21 AAC99558 Upstream primer fo
c 994 11.4 54.3 86 21 AAC99730 Upstream primer fo
c 995 11.4 54.3 86 21 AAC99899 Upstream primer fo
c 996 11.4 54.3 86 21 AAC99958 Upstream primer fo
c 997 11.4 54.3 86 21 AAC60017 Upstream primer fo
c 998 11.4 54.3 86 21 AAC69076 Upstream primer fo
c 999 11.4 54.3 86 21 AAC69391 Upstream primer fo
c1000 11.4 54.3 86 21 AAC69447 Upstream primer fo

```

## ALIGNMENTS

## RESULT 1

ID AAZ92037 standard; DNA; 21 BP.

AAZ92037;

08-JUN-2000 (first entry)

STATS binding sequence oligonucleotide MGPe.

STAT5 protein; signal transducer and activator of transcription 5;  
protein binding sequence; transcription factor modulator; inhibitor;  
malignant cell removal; proliferative malignancy; neoplastic disease;  
immunological disorder; inflammatory disorder; therapy; ds.

Synthetic.

WO200006696-A2.

10-FEB-2000.

30-JUL-1999; 99WO-US17366.

30-JUL-1998; 98US-0094695.

XX

PA (UYSF-) UNIV SOUTH FLORIDA.

XX Zuckerman KS, Liu RY;

XX WPI; 2000-195281/17.

XX Therapeutic agent for treating transcription factor-related illnesses

PT such as proliferative malignancies, comprises an oligonucleotide for

PT regulating transcription factor function -

PS Claim 15; Page 34; 43pp; English.

XX This sequence represents a STAT5 (signal transducer and activator of

CC transcription 5) protein binding effective amount of an oligonucleotide

CC (1) for modulating the function of transcription factors and a

CC pharmaceutical acceptable carrier. The oligonucleotides can be used in a

CC method of removing malignant cells in vitro. The oligonucleotides can be

CC used in compositions to inhibit transcription factors in illnesses where

CC transcription factors play a role, especially proliferative malignancies,

CC neoplastic diseases, and immunological and inflammatory disorders.

XX Sequence 21 BP; 8 A; 3 C; 3 G; 7 T; 0 other;

SQ

Query Match 100.0%; Score 21; DB 21; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGATTCTACGAATTCATTC 21

DB 1 AGATTCTACGAATTCATTC 21

RESULT 2

AAV46012 standard; DNA; 20 BP.

AAV46012;

16-OCT-1998 (first entry)

Immune adjuvant STAT5.

Immune system; adjuvant; vaccine; cancer; prophylactic; pathogenicity;

modulator; tolerance; regulator; helper cell; antigen; immunoglobulin;

Ig class; autoimmune response; T-cell; B-cell; tumour; ss.

Class Bacteria.

EP855184-A1.

23-JAN-1997; 97EP-0101019.

23-JAN-1997; 97EP-0101019.

(HEEG/) HEEG K.

(LIPF/) LIPFORD G B.

(WAGN/) WAGNER H.

Heeg K, Lipford GB, Wagner H;

WPI; 1998-389630/34.

Antigenic composition comprises polynucleotide fragment and antigen

PT - used as vaccine to treat or prevent e.g. cancer or pathogen

PT infections and to modulate immune response e.g. tolerance break and

PT regulation of TH1/TH2 cells

Example 5; Page 9; 28pp; English.

AAV45993-V46019 are fragments of bacterial polynucleotides which are

CC used as immune adjuvants for inclusion into vaccines to treat cancer and  
CC for prophylaxis and/or treatment of conditions caused by pathogenic  
CC micro-organisms. The polynucleotide is used for modulation of an immune  
CC response and the modulation is selected from the group break of  
CC tolerance, regulation of TH1/TH2 helper cell responses, switch of Ig  
CC classes, treatment of autoimmune responses and induction of tolerances.  
CC DNA oligomers are used to enhance the reactivity of immune cells to  
CC viral, bacterial and parasitic antigens, to break tolerance in anergic T  
CC and B cells e.g. against tumour antigens, as adjuvants in vaccination  
CC against tumour-defined antigens and immunostimulatory substances in an  
CC immune response against tumours and to suppress immune reactions of the  
CC innate and acquired immune system. The composition is inexpensive and  
CC stable and does not cause lethal shock, which happens with prior art  
CC bacterial sequences.

CC SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 other;

Query Match 85.7%; Score 18; DB 19; Length 20;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCAA 18  
DB 1 AGATTCTAGGAATTCAA 18

RESULT 3  
ID AAL39155 standard; DNA; 20 BP.

AC AAL39155;

DT 05-SEP-2002 (first entry)

DE Murine Toll-like receptor related Cpg DNA SEQ ID No 30.

KM Murine Toll-like receptor; TLR9; TLR8; ISNA; ds.

OS Unidentified.

PN WO200222809-A2.

PD 21-MAR-2002.

PF 17-SEP-2001; 2001WO-US29229.

PR 15-SEP-2000; 2000US-233035P.

PR 23-JAN-2001; 2001US-263657P.

PR 17-MAY-2001; 2001US-291726P.

PR 22-JUN-2001; 2001US-300210P.

PA (COLE-) COLEY PHARM GMBH.

PI Bauer S, Liford G, Wagner H;

PT WPI; 2002-393964/42.

PS Disclosure; Page 76; 195pp; English.

CC The invention relates to isolated murine Toll-like receptors (TLR) 9,  
CC TLR7 and TLR8 polypeptides. These polypeptides comprise fully defined  
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or  
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their  
CC fragments have an amino acid sequence which is identical to human TLR9,  
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino  
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the  
CC invention are useful for inhibiting TLR9 signalling activity in a cell.  
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid  
CC molecules which interact with a TLR polypeptide or its fragment. The

CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The  
CC signalling activity of a test compound (that is not a nucleic acid, and  
CC is a polypeptide or a part of a combinatorial library of compounds) with  
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for  
CC identifying species specificity of an ISNA. The isolated nucleic acids of  
CC the invention are useful as probes or primers. This polynucleotide  
CC sequence represents DNA relating to the isolated Toll-like receptors of  
CC the invention.

CC SQ Sequence 20 BP; 7 A; 3 C; 3 G; 7 T; 0 other;

Query Match 85.7%; Score 18; DB 24; Length 20;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCAA 18  
DB 1 AGATTCTAGGAATTCAA 18

RESULT 4  
ID ABT17264 standard; DNA; 21 BP.

AC ABT17264;

DT 10-APR-2003 (first entry)

DE Transcription factor probe - SEQ ID No 91.

KM Probe; ss; transcription factor-protein complex; transcription factor;  
KM drug screening; drug identification; array hybridisation.

OS Unidentified.

PN WO2002101351-A2.

PD 19-DEC-2002.

PF 30-MAY-2002; 2002WO-US17408.

PR 08-JUN-2001; 2001US-0877243.

PR 08-JUN-2001; 2001US-0877403.

PR 08-JUN-2001; 2001US-0877705.

PR 05-SEP-2001; 2001US-0947274.

PA (PANO-) PANOMICS INC.

PI Li X;

PT WPI; 2003-148829/14.

CC Identifying transcription factor-protein complexes, by isolating  
CC transcription factor complexes from sample based on a specific type of  
CC factor, and identifying different proteins present in isolated  
CC complexes

PS Disclosure; Fig 6; 167pp; English.

CC The invention comprises a method for identifying complexes between a  
CC transcription factor and another protein. The invention also comprises a  
CC method for isolating DNA probes which bind to activated transcription  
CC factors. The methods of the invention are useful for identifying  
CC transcription factor-protein interactions. The methods of the invention  
CC are also useful for facilitating the screening and identification of new  
CC drugs, characterising their mechanism of action and screening for adverse  
CC side effects based on drug's impact expression. The present DNA sequence  
CC represents a probe used in the method of the invention.

CC SQ Sequence 21 BP; 7 A; 4 C; 3 G; 7 T; 0 other;

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Query Match      85.7%; Score 18; DB 25; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
        |||
        1 AGATTCTAGGAATTCAA 18
Db

RESULT 5
ABT17265/c
ID      ABT17265 standard; DNA; 21 BP.
XX
AC      ABT17265;
XX
DT      10-APR-2003 (first entry)
XX
DE      Transcription factor probe - SEQ ID No 92.
XX
KM      Probe; ss: transcription factor-protein complex; transcription factor;
XX      drug screening; drug identification; array hybridisation.
XX      Unidentified.
XX      WO2002101351-A2.
XX      19-DEC-2002.
XX      30-MAY-2002; 2002WO-US17408.
XX
PR      08-JUN-2001; 2001US-0877243.
PR      08-JUN-2001; 2001US-0877403.
PR      08-JUN-2001; 2001US-0877705.
PR      08-JUN-2001; 2001US-0877738.
PR      05-SEP-2001; 2001US-0947274.
XX
PA      (PANO-) PANOMICS INC.
XX
PI      L1 X;
XX
DR      WPI; 2003-148829/14.
XX
PT      Identifying transcription factor-protein complexes, by isolating
PT      transcription factor complexes from sample based on a specific type of
PT      factor, and identifying different proteins present in isolated
PT      complexes -
XX
PS      Disclosure; Fig 6; 167bp; English.
XX
CC      The invention comprises a method for identifying complexes between a
CC      transcription factor and another protein. The invention also comprises a
CC      method for isolating DNA probes which bind to activated transcription
CC      factors. The methods of the invention are useful for identifying
CC      transcription factor-protein interactions. The methods of the invention
CC      are also useful for facilitating the screening and identification of new
CC      drugs, characterising their mechanism of action and screening for adverse
CC      side effects based on drug's impact expression. The present DNA sequence
CC      represents a probe used in the method of the invention.
XX
SQ      Sequence 21 BP; 7 A; 3 C; 4 G; 7 T; 0 other;

Query Match      85.7%; Score 18; DB 25; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
        |||
        21 AGATTCTAGGAATTCAA 4
Db

RESULT 6
ABT17327/c
ID      ABT17327 standard; DNA; 63 BP.
XX
AC      ABT17327;
XX
DT      10-APR-2003 (first entry)
XX
DE      Transcription factor-related array hybridisation probe - SEQ ID No 154.
XX
KM      Probe; ss: transcription factor-protein complex; transcription factor;
XX      drug screening; drug identification; array hybridisation.
XX      Unidentified.
XX      WO2002101351-A2.
XX      19-DEC-2002.
XX      30-MAY-2002; 2002WO-US17408.
XX
PR      08-JUN-2001; 2001US-0877243.
PR      08-JUN-2001; 2001US-0877403.
PR      08-JUN-2001; 2001US-0877705.
PR      08-JUN-2001; 2001US-0877738.
PR      05-SEP-2001; 2001US-0947274.
XX
PA      (PANO-) PANOMICS INC.
XX
PI      L1 X;
XX
DR      WPI; 2003-148829/14.
XX
PT      Identifying transcription factor-protein complexes, by isolating
PT      transcription factor complexes from sample based on a specific type of
PT      factor, and identifying different proteins present in isolated
PT      complexes -
XX
PS      Disclosure; Fig 6; 167bp; English.
XX
CC      The invention comprises a method for identifying complexes between a
CC      transcription factor and another protein. The invention also comprises a
CC      method for isolating DNA probes which bind to activated transcription
CC      factors. The methods of the invention are useful for identifying
CC      transcription factor-protein interactions. The methods of the invention
CC      are also useful for facilitating the screening and identification of new
CC      drugs, characterising their mechanism of action and screening for adverse
CC      side effects based on drug's impact expression. The present DNA sequence
CC      represents a probe used in the method of the invention.
XX
SQ      Sequence 63 BP; 21 A; 9 C; 12 G; 21 T; 0 other;

Query Match      85.7%; Score 18; DB 25; Length 63;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
        |||
        63 AGATTCTAGGAATTCAA 46
Db

RESULT 7
AAAS4479
ID      AAAS4479 standard; DNA; 100 BP.
XX
AC      AAAS4479;
XX
DT      11-APR-2001 (first entry)
XX
DE      DNA fragment comprising STAT transcription factors.
XX
KM      zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
KM      binding; detection; modulation; recombinant cell; lymph;
KM      haematopoietic cell; lymphoid cell; myeloid cell; lymph;
KM      immune system; blood; bone; inflammatory response; inflammation;
KM      spleen; human; primer; ss.

```

```

XX OS Synthetic.
XX PN WO200068381-A1.
XX PD 16-NOV-2000.
XX PF 11-MAY-2000; 2000WO-US12924.
XX PR 11-MAY-1999; 99US-0309861.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX DR WPI; 2001-016096/02.
XX PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
XX PT that stimulate proliferation or development of haematopoietic,
XX PT lymphoid and myeloid cells
XX PS
XX PS Example 19; Page 128; 134pp; English.
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. Those cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. An exemplary luciferase
CC mammalian expression vector is the K2134 plasmid which was
CC constructed with two complementary oligonucleotides (AAAs4479,
CC AAAs4480) which comprise STAT transcription factors from 4 genes
CC (a modified c-fos 5'is element, the p21 SIB1 from the p21 WAI1
CC gene, the mammary gland response element of the beta-casein gene
CC and a STAT inducible element of the Fcg RI gene.
XX
XX SQ Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;
XX
XX Query Match 85.7%; Score 18; DB 22; Length 100;
XX Best Local Similarity 100.0%; Pred. No. 76;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGATTCTAGGAATTCAA 18
OY ||||||||||||||||
DB 67 AGATTCTAGGAATTCAA 84

```

RESULT 8  
AAAs4480/c  
ID AAAs4480 standard; DNA; 100 BP.  
XX  
AC AAAs4480;  
XX  
DT 11-APR-2001 (first entry)  
XX  
DE DNA fragment comprising STAT transcription factors.  
XX  
KW zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;  
KW binding; detection; modulation; recombinant cell;  
KW haematopoietic cell; lymphoid cell; myeloid cell; lymph;  
KW immune system; blood; bone; inflammatory response; inflammation;  
KW spleen; human; primer; ss.

```

XX OS Synthetic.
XX PN WO200068381-A1.
XX PD 16-NOV-2000.
XX PF 11-MAY-2000; 2000WO-US12924.
XX PR 11-MAY-1999; 99US-0309861.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Presnell SR, Foster DC, Hammond AK, Lok S;
XX DR WPI; 2001-016096/02.
XX PT New cytokine receptor mouse zcytor 10, useful for detecting ligands
XX PT that stimulate proliferation or development of haematopoietic,
XX PT lymphoid and myeloid cells
XX PS
XX PS Example 19; Page 128; 134pp; English.
CC Isolating a nucleotide which encodes the zcytor 10 cytokine
CC receptor enables the production of recombinant cells expressing the
CC receptor. Those cells can then be used to detect the presence of a
CC modulator of zcytor10 protein by culturing the cells in the presence
CC of a test ligand and comparing levels of activity of mouse zcytor10
CC in the presence and absence of the test sample. Similarly, detection
CC of zcytor10 receptor ligand within a test sample can be achieved.
CC The method comprising contacting a test sample containing an amino
CC acid sequence from Cys15 or Gly25 to Pro230 of the zcytor 10
CC cytokine receptor and detecting the binding of the polypeptide to a
CC ligand in the sample. Specified peptide fragments of the zcytor 10
CC cytokine receptor and the methods described are used to identify
CC ligands that stimulate the proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells. Peptide fragments of
CC the cytokine receptor are useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders and for generating
CC antibodies directed against the receptor. An exemplary luciferase
CC mammalian expression vector is the K2134 plasmid which was
CC constructed with two complementary oligonucleotides (AAAs4479,
CC AAAs4480) which comprise STAT transcription factors from 4 genes
CC (a modified c-fos 5'is element, the p21 SIB1 from the p21 WAI1
CC gene, the mammary gland response element of the beta-casein gene
CC and a STAT inducible element of the Fcg RI gene.
XX
XX SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;
XX
XX Query Match 85.7%; Score 18; DB 22; Length 100;
XX Best Local Similarity 100.0%; Pred. No. 76;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGATTCTAGGAATTCAA 18
OY ||||||||||||||||
DB 38 AGATTCTAGGAATTCAA 21

```

RESULT 9  
ABA93801  
ID ABA93801 standard; DNA; 100 BP.  
XX  
AC ABA93801;  
XX  
DT 01-MAY-2002 (first entry)  
XX  
DE K2134 plasmid construction oligonucleotide SEQ ID NO:43.  
XX  
KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;  
KW antinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;  
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
KW infection; immunosuppression; cytotoxicity; leukaemia; Crohn's disease;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;

KM		inflammatory disease; pancreatitis; inflammatory bowel disease;
KW		PCR primer; probe; ss.
XX		Synthetic.
OS		
PN		WO200200721-A2.
PD		
XX		03-JAN-2002.
XX		
PF		26-JUN-2001; 2001WO-US20484.
PR		26-JUN-2000; 2000US-214282P.
ER		29-JUN-2000; 2000US-214955P.
XX		08-FEB-2001; 2001US-267963P.
PA		(ZYMO ) ZYMOGENETICS INC.
PI		Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JW,
PI		Marrer MF;
DR		WP1; 2002-C-090519/12.
XX		
PT		Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT		useful for treating and diagnosing lymphoid, immune, inflammatory,
PT		splenic, blood or bone disorders -
XX		
PS		Example 19; Page 190; 235pp; English.
CC		The present invention describes a cytokine receptor designated zcytor17.
CC		Zcytor17 has immunomodulatory, anti-inflammatory, antiviral, cytostatic,
CC		antineumatic, antirheitic and muscular activities. The zcytor17
CC		proteins are useful for treating and diagnosing lymphoid, immune,
CC		inflammatory, splenic, blood or bone disorders. Agonists or
CC		anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC		immunity and for stimulating lymphocyte proliferation, such as in the
CC		treatment of infections involving immunosuppression, including certain
CC		viral infections. They are also useful for inducing cytotoxicity and
CC		for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC		for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC		sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC		pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC		chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC		ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC		embodiment of the present invention.
XX		
SQ		Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;
		Query Match            85.7%;     Score 18;     DB 24;     Length 100;
		Best Local Similarity    100.0%;   Pred. No. 76;
		Matches    18;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
Oy		1 AGATTCTGAGAAATTCGA 18
Dd	67 AGATTCTGAGAAATTCGA 84	
		RESULT 10
		ABA93802/c
ID		ABA93802 standard; DNA; 100 BP.
XX		
AC		ABA93802;
XX		
DT		01-MAY-2002 (first entry)
XX		
DE		KZ134 plasmid construction oligonucleotide SEQ ID NO:44.
XX		
KW		Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW		anti-inflammatory; antiviral; antitumoric; antiarthritis; cytostatic;
KW		mucular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW		infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW		autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW		inflammatory disease; pancreatitis; inflammatory bowel disease;
KW		PCR primer; probe; ss.

```

XX OS Synthetic.
XX PN WO200200721-A2.
XX PD 03-JAN-2002.
XX PF 26-JUN-2001, 2001WO-US20484.
XX PR 26-JUN-2000; 2000US-214282P.
XX PR 29-JUN-2000; 2000US-21455P.
XX PR 08-FEB-2001; 2001US-267963P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
XX PI Maurer MF;
XX XX WPI, 2002-090519/12.
XX DR
XX PR Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
XX PR useful for treating and diagnosing lymphoid, immune, inflammatory,
XX PR splenic, blood or bone disorders -
XX XX
XX PS Example 19; Page 190; 235pp; English.
XX CC
XX CC The present invention describes a cytokine receptor designated zcytor17.
XX CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
XX CC antirheumatic, antirheptic and muscular activities. The zcytor17
XX CC proteins are useful for treating and diagnosing lymphoid, immune,
XX CC inflammatory, splenic, blood or bone disorders. Agonists or
XX CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
XX CC immunity and for stimulating lymphocyte proliferation, such as in the
XX CC treatment of infections involving immunosuppression, including certain
XX CC viral infections. They are also useful for inducing cytotoxicity and
XX CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
XX CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
XX CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
XX CC psoriasis, and inflammatory bowel disease. Zcytor17 was mapped to
XX CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
XX CC ABA93983 and ABB05730 to ABB05745 represent sequences used in the
XX CC exemplification of the present invention.
XX CC
XX SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;
XX
XX Query Match 85.7%; Score 18; DB 24; Length 100;
XX Best local Similarity 100.0%; Pred. No. 76;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AGATTTCTAGGAAATTCAA 18
XX |||||
XX |||||
XX DB 38 AGATTTCTAGGAAATTCAA 21
XX
XX RESULT 11
XX ID AAS20691
XX AC AAS20691 standard; DNA; 100 BP.
XX XX
XX XX 09-APR-2002 (first entry)
XX DE Plasmid K2 134 oligonucleotide ZC12749.
XX XX
XX KW Cytokine; zaphal ligand; zaphal1 receptor; NK cell progenitor;
XX KW natural killer cell proliferation; T-cell proliferation;
XX KW B-cell proliferation; anti-tumour response; immune system;
XX KW immunostimulant; cyostatic; primer; ss.
XX OS Synthetic.
XX XX
XX XX US6307024-B1.
XX PN

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PD 23-OCT-2001.  
XX  
XX 09-MAR-2000; 2000US-0522217.  
PF  
XX 09-MAR-1999; 99US-123547P.  
PR 11-MAR-1999; 99US-123804P.  
PR 01-JUL-1999; 99US-142013P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;  
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
DR WPI; 2002-040208/05.  
XX  
XX New zalphall ligand polypeptides and polynucleotides, useful for  
PT stimulating proliferation, activation, differentiation and/or induction  
PT of inhibition of specialized cell function, or for stimulating an  
PT antigenic response -  
XX  
XX Example 20; Column 149-150; 105pp; English.  
XX  
XX The present invention relates to the isolation of a novel cytokine,  
CC zalphall ligand and the polynucleotide encoding it. The invention  
CC also gives the sequence for the zalphall receptor and the polynucleotide  
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of  
CC natural killer (NK) cells or NK cell progenitors, the activation of NK  
CC cells, proliferation of T-cells, proliferation of B-cells stimulated  
CC with anti-CD40 antibodies, stimulates an antigenic response in a mammal,  
CC and reduces proliferation of B-cells stimulated with anti-IgM antibodies.  
CC The zalphall ligand polypeptide is also useful in preparing antibodies  
CC that bind to zalphall ligand epitopes. The zalphall ligand  
CC polynucleotides can be used as probes or primers to clone regions  
CC of a zalphall ligand gene, and in gene therapy. Zalphall ligand may  
CC also be used to identify inhibitors of its activity, to enhance the  
CC generation of anti-tumour responses with or without the infusion of  
CC donor lymphocytes, and to activate or stimulate the immune system.  
CC The present sequence represents an oligonucleotide used to construct  
CC plasmid KZ 134 in the methods of the present invention.  
XX  
SQ Sequence 100 BP; 25 A; 32 C; 17 G; 26 T; 0 other;  
XX  
Query Match 85.7%; Score 18; DB 24; Length 100;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AGATTTCGAGAAATTCAA 18  
DB 67 AGATTTCGAGAAATTCAA 84  
RESULT 12  
AAS20692/c  
ID AAS20692 standard; DNA; 100 BP.  
AC AAS20692;  
XX  
XX 09-APR-2002 (first entry)  
DT  
XX  
XX Plasmid KZ 134 oligonucleotide ZC12748.  
DE  
XX  
XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;  
KM natural killer cell proliferation; T-cell proliferation;  
KM B-cell proliferation; anti-tumour response; immune system;  
KM immunostimulant; cytostatic; primer; ss.  
XX  
XX Synthetic.  
OS  
XX US6307024-B1.  
XX  
XX 23-OCT-2001.  
PD  
XX  
XX 09-MAR-2000; 2000US-0522217.  
PF

XX  
XX 09-MAR-1999; 99US-123547P.  
PR 11-MAR-1999; 99US-123804P.  
PR 01-JUL-1999; 99US-142013P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;  
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
DR WPI; 2002-040208/05.  
XX  
XX New zalphall ligand polypeptides and polynucleotides, useful for  
PT stimulating proliferation, activation, differentiation and/or induction  
PT of inhibition of specialized cell function, or for stimulating an  
PT antigenic response -  
XX  
XX Example 20; Column 149-151; 105pp; English.  
XX  
XX The present invention relates to the isolation of a novel cytokine,  
CC zalphall ligand and the polynucleotide encoding it. The invention  
CC also gives the sequence for the zalphall receptor and the polynucleotide  
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of  
CC natural killer (NK) cells or NK cell progenitors, the activation of NK  
CC cells, proliferation of T-cells, proliferation of B-cells stimulated  
CC with anti-CD40 antibodies, stimulates an antigenic response in a mammal,  
CC and reduces proliferation of B-cells stimulated with anti-IgM antibodies.  
CC The zalphall ligand polypeptide is also useful in preparing antibodies  
CC that bind to zalphall ligand epitopes. The zalphall ligand  
CC polynucleotides can be used as probes or primers to clone regions  
CC of a zalphall ligand gene, and in gene therapy. Zalphall ligand may  
CC also be used to identify inhibitors of its activity, to enhance the  
CC generation of anti-tumour responses with or without the infusion of  
CC donor lymphocytes, and to activate or stimulate the immune system.  
CC The present sequence represents an oligonucleotide used to construct  
CC plasmid KZ 134 in the methods of the present invention.  
XX  
SQ Sequence 100 BP; 26 A; 17 C; 32 G; 25 T; 0 other;  
XX  
Query Match 85.7%; Score 18; DB 24; Length 100;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AGATTTCGAGAAATTCAA 18  
DB 38 AGATTTCGAGAAATTCAA 21  
RESULT 13  
AAD22953  
ID AAD22953 standard; DNA; 100 BP.  
AC AAD22953;  
XX  
XX 26-FEB-2002 (first entry)  
DT  
XX  
XX Bar3/KZ134/zalphall cell line constructing ZC12,749 oligonucleotide.  
DE  
XX  
XX Zalphall; cytokine receptor; immunosuppressive; cytostatic; haemostatic;  
KM inflammatory disorder; cell proliferation; immune disorder; cancer; SLE;  
KM systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis;  
KM diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;  
KM inflammatory bowel disease; sepsis; Crohn's disease; viral infection;  
KM asthma; ss.  
XX  
XX Unidentified.  
OS  
XX WO200177171-A2.  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 03-APR-2001; 2001WO-US10872.  
PF

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PR 05-APR-2000; 2000US-194731P.
PR 28-JUL-2000; 2000US-222121P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
XX WPI; 2002-025898/03.
XX
PT Novel soluble receptor polypeptides and polynucleotides used as
PT cytokine antagonist for stimulating ligand activity-induced
PT proliferation of hematopoietic cells and for suppressing immune
PT response in a mammal
XX
PS Example 19; Page 213; 243pp; English.
XX
CC The invention relates to an isolated soluble zalphail cytokine receptor
CC polypeptide and their cDNA molecules. Zalphail proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC hematopoietic cells and hematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalphail is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalphail is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is an oligonucleotide used for Baf3/KZ134/zalphail cell line
CC construction.
XX
SQ Sequence 100 BP; 24 A; 33 C; 17 G; 26 T; 0 other;

Query Match      85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCOA 18
DB 67 AGATTCTAGGAATTCOA 84

RESULT 14
AAD22954/c
ID AAD22954 standard; DNA; 100 BP.
XX
AC AAD22954;
XX
DT 26-FEB-2002 (first entry)
XX
DE Baf3/KZ134/zalphail cell line constructing ZC12,748 oligonucleotide.
XX
KW Zalphail; cytokine receptor; immunosuppressive; cytostatic; hemostatic;
KW inflammatory disorder; cell proliferation; immune disorder; cancer; SLE;
KW systemic lupus erythematosus; myasthenia gravis; rheumatoid arthritis;
KW diabetes; autoimmune disease; multiple sclerosis; ulcerative colitis;
KW inflammatory bowel disease; sepsis; Crohn's disease; viral infection;
KW asthma; ss.
XX
OS Unidentified.
XX
PN WO200177171-A2.
XX
PD 18-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US10872.
XX
PR 05-APR-2000; 2000US-194731P.
XX
PR 28-JUL-2000; 2000US-222121P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX

```

```

PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;
XX WPI; 2002-025898/03.
XX
PT Novel soluble receptor polypeptides and polynucleotides used as
PT cytokine antagonist for stimulating ligand activity-induced
PT proliferation of hematopoietic cells and for suppressing immune
PT response in a mammal
XX
PS Example 19; Page 213; 243pp; English.
XX
CC The invention relates to an isolated soluble zalphail cytokine receptor
CC polypeptide and their cDNA molecules. Zalphail proteins are useful for
CC inhibiting or antagonising the ligand activity-induced proliferation of
CC hematopoietic cells and hematopoietic cell progenitors preferably
CC lymphoid cells which are natural killer cells or cytotoxic T cells.
CC Zalphail is useful for treating immune and inflammatory disorders, for
CC reducing proliferation of neoplastic B or T cells, for suppressing an
CC immune response in a mammal exposed to an antigen or pathogen. Zalphail is
CC useful for treating diseases that require immune regulation including
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,
CC sepsis, viral infection (dengue virus infection) and cancer. The present
CC sequence is an oligonucleotide used for Baf3/KZ134/zalphail cell line
CC construction.
XX
SQ Sequence 100 BP; 26 A; 17 C; 33 G; 24 T; 0 other;

Query Match      85.7%; Score 18; DB 24; Length 100;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCOA 18
DB 38 AGATTCTAGGAATTCOA 21

RESULT 15
ABK88204/c
ID ABK88204 standard; DNA; 33 BP.
XX
AC ABK88204;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human cytochrome bcl core protein cDNA specific PCR primer #2.
XX
KW Cytochrome bcl; primer; ss; core protein IT12. 21; cancer; HIV;
KW human immunodeficiency virus; human; PCR.
XX
OS Homo sapiens.
XX
PN CN1340524-A.
XX
PD 20-MAR-2002.
XX
PF 31-AUG-2000; 2000CN-0119831.
XX
PR 31-AUG-2000; 2000CN-0119831.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
PD WPI; 2002-436418/47.
XX
PF Polypeptide-human cytochrome bcl compound core protein II 12.21 and
PT polynucleotide for coding it -
XX
PS Example 4; Page 19 (disclosure); 34pp; Chinese.
XX
CC This invention relates to the cDNA and protein sequences of a novel

```

CC polypeptide-human cytochrome bcl compounds core protein I112.21. The  
 CC invention also comprises a method for producing the protein by  
 CC recombinant DNA technology and a method for the application of the  
 CC polypeptide in treating diseases such as cancer, HIV infection, etc.  
 CC The invention also discloses an antagonist against this polypeptide and  
 CC its therapeutic action, and the application of the polynucleotide to  
 CC coding this new human cytochrome bcl compound core protein I112.21.  
 CC The present sequence represents a PCR primer used to clone the human  
 CC cytochrome bcl compound core protein I112.21 cDNA of the invention.

XX Sequence 33 BP; 10 A; 10 C; 4 G; 9 T; 0 other;

Query Match 76.2%; Score 16; DB 24; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTC 16  
 |||||  
 DB 19 AGATTCTAGGAATTC 4

#### RESULT 16

ABL31609  
 ID AAL31609 standard; DNA; 51 BP.

AC AAL31609;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #4817.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinase; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI, 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 CC oncogenes and histones, useful for diagnosing and treating, e.g.

PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 2773; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
 CC histones, kinases, colony stimulating factors, complement related  
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,  
 CC G-protein coupled receptors and thioesterases. The present sequence is  
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
 CC by them may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate expression of the proteins listed  
 CC above. Disorders that may be prevented, diagnosed and/or treated include

CC multifactorial diseases with a genetic component, such as autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,  
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.

XX Sequence 51 BP; 22 A; 6 C; 8 G; 15 T; 0 other;

Query Match 73.3%; Score 15.4; DB 22; Length 51;  
 Best Local Similarity 94.1%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ATTTCTAGGAATTC 19  
 |||||  
 DB 9 ATTTCTAGGAATTC 25

#### RESULT 17

ABL53039/c  
 ID ABL53039 standard; DNA; 41 BP.

AC ABL53039;

DT 29-MAY-2002 (first entry)

DE Oligonucleotide JCA 325.

XX Virucide; vaccine; foot and mouth disease; P1 region; capsid;  
 KW 3C protease; ds.

XX Foot and mouth disease virus.

OS WO200200251-A1.

PN 03-JAN-2002.

PD 27-JUN-2001; 2001WO-FR02042.

PF 29-JUN-2000; 2000FR-0008437.

PR (MERI-) MERIAL.

PI King A, Burman A, Audonnet J, Lombard M;

DR WPI, 2002-130837/17.

PT Stable, potent effective vaccines against foot-and-mouth disease,  
 CC comprises recombinantly produced empty virus capsids as antigens -

PS Example 7; Page 29; 79pp; French.

XX The present invention relates to a vaccine against foot and mouth disease  
 CC (FMD) comprising (in addition to a veterinary vehicle or excipient) an  
 CC antigen consisting of empty FMD virus capsids, obtained by expression in  
 CC eukaryotic cells of the cDNA of the following regions of the FMD genome:  
 CC the P1 region encoding the capsid and the region encoding the 3C  
 CC protease. The vaccine is effective, reliable and stable, and is effective  
 CC at low doses. The vaccine is useful against foot and mouth disease,  
 CC especially in cows, sheep, pigs or goats. The present sequence is an  
 CC oligonucleotide which was used in an example from the invention.

XX Sequence 41 BP; 13 A; 7 C; 6 G; 15 T; 0 other;

Query Match 70.5%; Score 14.8; DB 24; Length 41;  
 Best Local Similarity 88.9%; Pred. No. 2.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTTCTAGGAATTC 19  
 |||||  
 DB 19 GATTTCTAGGAATTC 2

```

RESULT 18
ABL53041/c
ID ABL53041 standard; DNA; 41 BP.
XX
XX
AC ABL53041;
XX
XX 29-MAY-2002 (first entry)
XX
XX Oligonucleotide JCA 327.
DE
XX virucide; vaccine; foot and mouth disease; P1 region; capsid;
XX 3C protease; ds.
XX
XX Foot and mouth disease virus.
XX
XX WO200200251-A1.
XX
XX 03-JAN-2002.
XX
XX 27-JUN-2001; 2001WO-FR02042.
XX
XX 29-JUN-2000; 2000FR-0008437.
XX
XX (MERI-) MERTAL.
XX
XX King A, Burman A, Audonnet J, Lombard M;
XX
XX WPI; 2002-130837/17.
XX
XX Stable, potent effective vaccines against foot-and-mouth disease,
XX comprises recombinantly produced empty virus capsids as antigens
XX
XX Example 7; Page 30; 79pp; French.
XX
XX The present invention relates to a vaccine against foot and mouth disease
XX (FMD) comprising (in addition to a veterinary vehicle or excipient) an
XX antigen consisting of empty FMD virus capsids, obtained by expression in
XX eukaryotic cells of the cDNA of the following regions of the FMD genome:
XX the P1 region encoding the capsid and the region encoding the 3C
XX protease. The vaccine is effective, reliable and stable, and is effective
XX at low doses. The vaccine is useful against foot and mouth disease,
XX especially in cows, sheep, pigs or goats. The present sequence is an
XX oligonucleotide which was used in an example from the invention.
XX
XX Sequence 41 BP; 13 A; 6 C; 6 G; 16 T; 0 other;
SQ
Query Match 70.5%; Score 14.8; DB 24; Length 41;
Best Local Similarity 88.9%; Pred. No. 2.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GATTTCAGGAATTCAAA 19
Db 19 GATTTTATGAAATTCAAA 2

```

```

XX
XX 27-JUN-2001; 2001WO-FR02042.
XX
XX 29-JUN-2000; 2000FR-0008437.
XX
XX (MERI-) MERTAL.
XX
XX King A, Burman A, Audonnet J, Lombard M;
XX
XX WPI; 2002-130837/17.
XX
XX Stable, potent effective vaccines against foot-and-mouth disease,
XX comprises recombinantly produced empty virus capsids as antigens
XX
XX Example 6; Page 26; 79pp; French.
XX
XX The present invention relates to a vaccine against foot and mouth disease
XX (FMD) comprising (in addition to a veterinary vehicle or excipient) an
XX antigen consisting of empty FMD virus capsids, obtained by expression in
XX eukaryotic cells of the cDNA of the following regions of the FMD genome:
XX the P1 region encoding the capsid and the region encoding the 3C
XX protease. The vaccine is effective, reliable and stable, and is effective
XX at low doses. The vaccine is useful against foot and mouth disease,
XX especially in cows, sheep, pigs or goats. The present sequence is an
XX oligonucleotide which was used in an example from the invention.
XX
XX Sequence 44 BP; 13 A; 7 C; 7 G; 17 T; 0 other;
SQ
Query Match 70.5%; Score 14.8; DB 24; Length 44;
Best Local Similarity 88.9%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GATTTCAGGAATTCAAA 19
Db 19 GATTTTATGAAATTCAAA 2

```

CC antigen consisting of empty FMD virus capsids, obtained by expression in  
CC eukaryotic cells of the cDNA of the following regions of the FMD genome:  
CC the P1 region encoding the capsid and the region encoding the 3C  
CC protease. The vaccine is effective, reliable and stable, and is effective  
CC at low doses. The vaccine is useful against foot and mouth disease,  
CC especially in cows, sheep, pigs or goats. The present sequence is an  
CC oligonucleotide which was used in an example from the invention.  
XX  
SQ Sequence 44 BP; 12 A; 10 C; 9 G; 13 T; 0 other;

Query Match 70.5%; Score 14.8; DB 24; Length 44;  
Best Local Similarity 88.9%; Pred. No. 2.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTTCCTAGCAATTCAAA 19  
19 GATTTCCTAGCAATTCAAA 2

Db 19 GATTTCCTAGCAATTCAAA 2

RESULT 21  
AAZ23234/c  
ID AAZ23234 standard; DNA; 46 BP.  
XX  
AC AAZ23234;  
XX  
DT 24-JAN-2000 (first entry)  
XX  
DE HCV NS5B gene amplifying nested primer.  
XX  
KW Hepatitis C virus; HCV; non-structural 5B; viral antigen; antiviral;  
KW immune response; diagnostic; therapeutic; pharmaceutical; NS5B;  
KW PCR primer; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
PN WO9951781-A1.  
XX  
PD 14-OCT-1999.  
XX  
PF 02-APR-1999; 99WO-US07404.  
XX  
PR 02-APR-1998; 98US-0080509.  
XX  
PR 23-JUN-1998; 98US-0090356.  
XX  
PA (VIRO-) VIROPHARMA INC.  
XX  
PI Collect MS;  
XX  
DR WPI; 1999-620215/53.  
XX  
PT Novel protein and polynucleotides used in diagnostic assays and  
PT therapeutic treatments for Hepatitis C virus -  
XX  
PS Example 1; Page 47; 129pp; English.  
XX  
SQ The invention provides nucleic acid molecules encoding hepatitis C virus  
CC (HCV) non-structural 5B (NS5B) proteins. The HCV NS5B protein can be  
CC used in assays to determine antagonistic or agonistic activity of test  
CC compounds against HCV. HCV can be detected in biological samples by  
CC amplification of the NS5B coding sequence and detection using an  
CC oligonucleotide probe (derived from the NS5B nucleotide sequence). The  
CC HCV NS5B protein is a viral antigen and can be used in raising an immune  
CC response in a mammalian subject. Cell lines comprising the HCV NS5B  
CC nucleic acid sequence can be used to assess the functionality of the  
CC protein and for assaying test compounds for antagonistic or agonistic  
CC activity. The HCV NS5B protein and nucleic acid sequences are useful in  
CC research, diagnostic, therapeutic and pharmaceutical applications, and  
CC for use in assays for the identification of efficacious antiviral  
CC agents. Sequences AAZ23232-235 represent PCR primers for cloning the HCV  
CC NS5B genes.  
XX  
SQ Sequence 46 BP; 17 A; 9 C; 6 G; 14 T; 0 other;

Query Match 69.5%; Score 14.6; DB 20; Length 46;  
Best Local Similarity 81.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTTCCTAGCAATTCAAATC 21  
25 ATATTTCCTAGCAATTCAGATC 5

Db 25 ATATTTCCTAGCAATTCAGATC 5

RESULT 22  
AAV59344  
ID AAV59344 standard; CDNA; 58 BP.  
XX  
AC AAV59344;  
XX  
DT 21-DEC-1998 (first entry)  
XX  
DE zsig10 primer ZC15.632.  
XX  
SS; human; mucous-mediated function; adhesion; tumour metastasis;  
KW bacterial colonisation; microbial infection; AIDS; cystic fibrosis;  
KW chronic obstructive pulmonary disease; asthma; Crohn's disease;  
KW sinonasal inflammatory disease; inflammatory bowel disease; bronchitis;  
KW PCR; primer; amplification.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9841627-A1.  
XX  
PD 24-SEP-1998.  
XX  
PF 18-MAR-1998; 98WO-US05251.  
XX  
PR 19-MAR-1997; 97US-0039631.  
XX  
PA (ZYMO) ZYMOGENETICS INC.  
XX  
PI Sheppard PO;  
XX  
DR WPI; 1998-531566/45.  
XX  
PT New isolated mucous-associated polypeptide, zsig10 - used to develop  
PT products for treating e.g. tumour metastasis, microbial infections,  
PT cystic fibrosis, asthma, bronchitis or inflammatory bowel disease  
XX  
PS Example 7; Page 94; 109pp; English.  
XX  
SQ The primers AAV59330-V59351 were used in the production of a human  
CC polypeptide zsig10. zsig10 is involved in mucous-mediated functions  
CC such as adhesion. The products of the invention can be used in the  
CC study and treatment of e.g. tumour metastasis, bacterial colonisation,  
CC susceptibility to and persistence of infection, microbial infections,  
CC AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma,  
CC sinonasal inflammatory disease, inflammatory bowel disease, bronchitis,  
CC or Crohn's disease. The products can also be used for detection,  
CC diagnosis and drug screening.  
XX  
SQ Sequence 58 BP; 17 A; 19 C; 9 G; 13 T; 0 other;

Query Match 69.5%; Score 14.6; DB 19; Length 58;  
Best Local Similarity 81.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTTCCTAGCAATTCAAATC 21  
14 AGAATCTAGCAATTCATCTC 34

Db 14 AGAATCTAGCAATTCATCTC 34

RESULT 23  
AAx80718  
ID AAx80718 standard; DNA; 58 BP.

```

XX AAX80718;
AC
XX
XX 28-SEP-1999 (first entry)
DE
XX Primer-5 for C-terminal CEE-Zalpalal linker synthesis.
XX
XX
XX Primer; human; alpha helical protein-1; Zalpalal; Fragile-X syndrome;
XX connective tissue; abnormal proliferative disorder; cancer;
XX cosmetic improvement; skin tone; elasticity; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9929720-A2.
XX
XX 17-JUN-1999.
XX
XX 10-DEC-1998; 98WO-US26273.
XX
XX 10-DEC-1997; 97US-0987926.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Conklin DC, Lok S, Parrish J;
XX
XX WPI; 1999-385572/32.
XX
XX Mammalian alpha helical protein-1, designated Zalpalal
XX
XX Example 6; Page 68; 73pp; English.
XX
XX The present sequence is an oligonucleotide which was used in PCR
XX for synthesis of C-terminal CEE-Zalpalal linker. The C-terminal
XX CEE-Zalpalal linker and N-terminal untagged linker were used for
XX construction of a CEE-Zalpalal plasmid which expressed the human alpha
XX helical protein. Zalpalal tagged with a Glu-Glu tag at the C-terminus in
XX Pichia methanolica. The Zalpalal protein may be useful in the treatment
XX of Fragile-X syndrome and abnormal proliferative disorders e.g. cancer.
XX It can also be used for the growth, differentiation, maintenance and
XX survival of connective tissues, particularly cardiovascular and epidermal
XX systems and in imparting cosmetic improvements to normal connective
XX tissues such as enhancement of skin tone and elasticity.
XX
XX Sequence 58 BP; 17 A; 19 C; 9 G; 13 T; 0 other;
XX
XX
XX Query Match 69.5%; Score 14.6; DB 20; Length 58;
XX Best Local Similarity 81.0%; Pred. No. 2.7e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 AGATTCTAGGAATTCATTC 21
XX |||||
XX 14 AGAATCTAGGAATTCATTC 34
XX
XX
XX RESULT 24
XX AAX24706
XX ID AAX24706 standard; DNA; 58 BP.
XX
XX AAX24706;
XX
XX 21-JUN-1999 (first entry)
XX
XX Linker primer ZC14819.
XX
XX Adipocyte-specific protein; zsig39; human; fatty acid metabolism;
XX energy balance; nutrition; antimicrobial; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO9910492-A1.
XX
XX 04-MAR-1999.
XX

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XX
XX 26-AUG-1998; 98WO-US17724.
XX
XX 26-AUG-1997; 97US-0056983.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Humes JM, Sheppard PO;
XX
XX WPI; 1999-204665/17.
XX
XX
XX Zsig39 protein - used to modulate fatty acid metabolism
XX
XX Example 8; 128; 132pp; English.
XX
XX Oligonucleotides ZC14819, ZC15267 (see AAX24705), ZC14820 (see
XX AAX24707) and ZC15273 (see AAX24704) were used in a PCR amplification
XX to generate an N-terminal untagged zsig39 linker. This was
XX utilised in the construction of a mammalian expression plasmid
XX for zsig39. Zsig39 (see AAW97984) is an adipocyte-specific protein
XX homologue that can be used to modulate fatty acid metabolism
XX (claimed). It may also be used in organ preservation, for
XX cryopreservation, for surgical pretreatment to prevent injury due
XX to ischaemia and/or inflammation, and as an antimicrobial agent.
XX
XX Sequence 58 BP; 17 A; 16 C; 9 G; 16 T; 0 other;
XX
XX
XX Query Match 69.5%; Score 14.6; DB 20; Length 58;
XX Best Local Similarity 81.0%; Pred. No. 2.7e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 AGATTCTAGGAATTCATTC 21
XX |||||
XX 14 AGAATCTAGGAATTCATTC 34
XX
XX
XX RESULT 25
XX AAS00972
XX ID AAS00972 standard; DNA; 58 BP.
XX
XX AAS00972;
XX
XX 16-JUL-2001 (first entry)
XX
XX PCR antisense common primer for C-terminal linker, no. 15632.
XX
XX C-terminal linker; plasmid construction; PCR primer;
XX homologous recombination; 15632; ss.
XX
XX Synthetic.
XX
XX US6207442-B1.
XX
XX 27-MAR-2001.
XX
XX 15-OCT-1998; 98US-0173043.
XX
XX 16-OCT-1997; 97US-0062061.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Raymond CK;
XX
XX WPI; 2001-256851/26.
XX
XX Preparing a double-stranded, circular DNA molecule, involves homologous
XX recombination of one or more donor DNA fragments encoding the protein
XX of interest, with an acceptor plasmid and DNA linkers in host cell -
XX
XX Example 1; Columns 25-26; 23pp; English.
XX
XX The sequence represents a PCR antisense common primer for a C-terminal
XX linker. The method of the invention comprises preparing a
XX

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RESULT 28
XX ABV72202/c
ID ABV72202 standard; DNA; 20 BP.
XX
AC ABV72202;
XX
DT 05-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a PCR primer.
XX
KW DNA fingerprint; phenotype; polymorphism; MITE; molecular marker;
XX miniature inverted repeat transposable element; PCR; primer; ss.
XX
OS Zea mays.
XX
PN US6420117-B1.
XX
PD 16-JUL-2002.
XX
PF 14-SEP-2000; 2000US-0662402.
XX
PR 14-SEP-1999; 99US-153812P.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI Messier SR, Casa AM;
XX
DR WPI; 2002-654638/70.
XX
PT Producing a DNA fingerprint of an individual by amplifying fragments
PT containing a miniature inverted repeat transposable element is useful
PT to detect polymorphisms and correlate genotype with phenotype
PT particularly in maize.
XX
PS Disclosure; Column 41; 37bp; English.
XX
CC The specification describes a method for producing a DNA fingerprint of
CC an individual. The method comprises generating restriction fragments to
CC which an adaptor is ligated, amplifying fragments containing a miniature
CC inverted repeat transposable element (MITE) and resolving the amplified
CC fragments. The presence of a certain amplified fragment is correlated
CC to a phenotype. The method is used to characterize the DNA of an
CC individual, to detect polymorphisms, to correlate presence of an
CC amplified fragment with phenotype and to generate a set of molecular
CC markers. The present PCR primer is used in the course of the invention.
XX
SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 other;

Query Match 67.6%; Score 14.2; DB 24; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCGAATC 21
Db 19 ATTTCGAGGAATTCGAATC 1

RESULT 29
XX AA164395/c
ID AA164395 standard; DNA; 27 BP.
XX
AC AA164395;
XX
DE 23-NOV-2001 (first entry)
XX
DE PCR primer #2.
XX
KW Green fluorescence protein; GFP; drug screening; PCR primer;
KW cell organelle formation; ss.
XX
OS Unidentified.

```

```

PN JP2001157588-A.
XX
PD 12-JUN-2001.
XX
PF 02-DEC-1999; 99JP-0343222.
XX
PR 02-DEC-1999; 99JP-0343222.
XX
PA (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.
XX
DR WPI; 2001-592442/67.
XX
PT Gene trap using a green fluorescence protein
XX
PS Example 1; Page 6; 17pp; Japanese.
XX
CC The present invention relates to a trap vector containing, from 5'- to
CC 3'-, an intron and splice acceptor sequence, a DNA sequence encoding
CC green fluorescence protein (GFP) in which methionine and valine at the
CC N-terminal are deleted, an internal ribosome binding site (IRES), a DNA
CC sequence encoding a selective marker, and polyadenylated signal sequence.
CC The invention can be used in the screening of drugs inhibiting or
CC promoting the formation of cell organelles. The present sequence is a PCR
CC primer, which was used in an example from the present invention.
XX
SQ Sequence 27 BP; 6 A; 6 C; 7 G; 8 T; 0 other;

Query Match 67.6%; Score 14.2; DB 22; Length 27;
Best Local Similarity 84.2%; Pred. No. 4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCGAA 19
Db 19 AGCTAGCTAGGAATTCGAA 1

RESULT 30
XX AA164405/c
ID AA164405 standard; DNA; 27 BP.
XX
AC AA164405;
XX
DE 23-NOV-2001 (first entry)
XX
DE PCR primer #12.
XX
KW Green fluorescence protein; GFP; drug screening; PCR primer;
KW cell organelle formation; ss.
XX
OS Unidentified.
XX
PN JP2001157588-A.
XX
PD 12-JUN-2001.
XX
PF 02-DEC-1999; 99JP-0343222.
XX
PR 02-DEC-1999; 99JP-0343222.
XX
PA (OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.
XX
DR WPI; 2001-592442/67.
XX
PT Gene trap using a green fluorescence protein
XX
PS Example 1; Page 7; 17pp; Japanese.
XX
CC The present invention relates to a trap vector containing, from 5'- to
CC 3'-, an intron and splice acceptor sequence, a DNA sequence encoding
CC green fluorescence protein (GFP) in which methionine and valine at the
CC N-terminal are deleted, an internal ribosome binding site (IRES), a DNA
CC sequence encoding a selective marker, and polyadenylated signal sequence.
CC The invention can be used in the screening of drugs inhibiting or

```



CC promoting the formation of cell organelles. The present sequence is a PCR  
CC primer, which was used in an example from the present invention.  
XX

Sequence 27 BP; 6 A; 6 C; 7 G; 8 T; 0 other;

Query Match 67.6%; Score 14.2; DB 22; Length 27;  
Best Local Similarity 84.2%; Pred. No. 4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAA 19  
DB 19 AGCTAGCTAGGAATTCAAA 1

RESULT 31

AA176494/c  
ID AA176494 standard; DNA; 51 BP.

AA176494;

09-NOV-2001 (first entry)

Human silent SNP containing nucleic acid SEQ:3435.

Human; single nucleotide polymorphism; SNP; genome; gene therapy;  
protein therapy; vaccine; probe; diagnostic assay; detection;  
quantitation; restorative therapy; polymorphic; ds.

Homo sapiens.

WO200140521-A2.

07-JUN-2001.

30-NOV-2000; 2000WO-US32758.

30-NOV-1999; 99US-0168138.

29-NOV-2000; 2000US-0726173.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-356160/37.

Polymorphic nucleic acid sequences, useful in genetic testing and  
therapy -

Claim 1; Page 1102; 2653pp; English.

AA173060 to AA179867 represent isolated human polymorphic polynucleotide  
sequences (I), which contain single nucleotide polymorphisms (SNPs).

AAW53114 to AAW53329 represent peptides related to human polymorphic  
polynucleotide sequences. The sequences can be used in gene and protein  
therapy, and in vaccine production. (I) and the polypeptides encoded by  
CC them may be used in the prevention, diagnosis and treatment of diseases  
associated with inappropriate expression of polymorphic polypeptides.  
For example, (I) may be used to treat disorders by rectifying mutations  
or deletions in a patient's genome that affect the activity of

CC polypeptides by expressing inactive proteins or to supplement the  
CC patients own production of polypeptide. Additionally, (I) and its  
CC complementary sequences may also be used as DNA probes in diagnostic

CC assays to detect and quantitate the presence of similar nucleic acids  
in samples, and therefore which patients may be in need of restorative  
CC therapy. The polypeptides encoded by (I) may be used as antigens in the  
CC production of antibodies specific for polymorphic polypeptides. The  
CC antibodies may also be used to down regulate expression and activity.

CC The antibodies may also be used as diagnostic agents for detecting the  
CC presence of polymorphic polypeptides in samples.

Sequence 51 BP; 17 A; 10 C; 3 G; 21 T; 0 other;

Query Match 67.6%; Score 14.2; DB 22; Length 51;

Best Local Similarity 84.2%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAAA 19  
DB 34 AGCTTTATAGGAATTCAAA 16

RESULT 32

AAC52964  
ID AAC52964 standard; DNA; 61 BP.

AAC52964;

18-OCT-2000 (first entry)

Arabidopsis thaliana DNA fragment SEQ ID NO: 72962.

Hybridisation assay; genetic mapping; gene expression control;  
protein identification; signal transduction pathway;  
metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

25-MAR-1999; 99US-0126264.

29-MAR-1999; 99US-0126785.

01-APR-1999; 99US-0127462.

06-APR-1999; 99US-0128234.

08-APR-1999; 99US-0129845.

16-APR-1999; 99US-0130077.

19-APR-1999; 99US-0130449.

21-APR-1999; 99US-0130510.

23-APR-1999; 99US-0130891.

28-APR-1999; 99US-0131449.

30-APR-1999; 99US-0132048.

30-APR-1999; 99US-0132407.

04-MAY-1999; 99US-0132484.

05-MAY-1999; 99US-0132485.

06-MAY-1999; 99US-0132486.

07-MAY-1999; 99US-0132487.

11-MAY-1999; 99US-0132863.

14-MAY-1999; 99US-0134218.

14-MAY-1999; 99US-0134219.

14-MAY-1999; 99US-0134221.

14-MAY-1999; 99US-0134370.

18-MAY-1999; 99US-0134768.

19-MAY-1999; 99US-0134941.

20-MAY-1999; 99US-0135124.

21-MAY-1999; 99US-0135353.

24-MAY-1999; 99US-0135629.

25-MAY-1999; 99US-0136021.

27-MAY-1999; 99US-0136392.

28-MAY-1999; 99US-0136782.

01-JUN-1999; 99US-0137222.

03-JUN-1999; 99US-0137528.

04-JUN-1999; 99US-0137502.

07-JUN-1999; 99US-0137724.

08-JUN-1999; 99US-0138094.

10-JUN-1999; 99US-0138540.

10-JUN-1999; 99US-0138647.

14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 23-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145182.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0146389.  
PR 04-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149930.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 22-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 67.6%; Score 14.2; DB 21; Length 61;  
Best Local Similarity 84.2%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCAA 19  
DB 36 AGATTCTAGGAACACAAA 54

```

RESULT 33
AAT86363/c
ID AAT86363 standard; DNA; 81 BP.
XX
AC AAT86363;
XX
DT 27-APR-1998 (first entry)
XX
DE C. krusei non-transcribed intergene region-derived probe F-beta.
XX
KW Non-transcribed intergene region; IGR; ribosome; cistron; 25S; 18S;
KW probe; hybridisation; detection; differentiation; yeast; diagnosis;
KW Geotrichum candidum, ss.
XX
OS Synthetic.
OS Candida krusei.
XX
XX Key Location/Qualifiers
FH repeat_region /*tag= a
FT repeat_unit 2..7
FH repeat_unit /*tag= b
FH
XX WO9736003-A1.
XX
XX 02-OCT-1997.
XX
XX 24-MAR-1997; 97WO-FR00518.
XX
XX 22-MAR-1996; 96FR-0003835.
XX
XX (INMR ) BIO MERIEUX.
XX
XX PA Carlotti A, Villard J;
XX
XX PI WPI; 1997-489661/45.
XX
XX DR
XX
XX PT Probe for detection and characterisation of yeast for diagnosis and
PT process control - comprises fragment derived from ribosomal DNA in
PT the non-transcribed intergene region that contains repeated
PT subsequences
XX
XX PS Claim 7; Page 30; 49pp; French.
XX
XX CC This is the sequence of probe F-alpha derived from the sequence of the
CC non-transcribed intergene region (IGR) F1 from Candida krusei
CC (AAT86363). The sequence is derived from a ribosomal cistron located in
CC the region between the 25S and 18S ribosomal DNA genes. Probes (see
CC AAT86362-T86365) derived from the IGR can be used for specific and/or
CC intraspecific detection, identification and/or differentiation of yeast
CC for medical diagnosis or for monitoring industrial processes,
CC specifically for Candida krusei and Geotrichum candidum.
XX
XX SQ Sequence 81 BP; 20 A; 5 C; 8 G; 48 T; 0 other;
XX
Query Match 67.6%; Score 14.2; DB 18; Length 81;
Best Local Similarity 84.2%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AGATTCTAGGAATTCAA 19
DB 65 AGATTCAAAAATTCAA 47

```

```

DE Human spliced transcript detection oligonucleotide SEQ ID NO:14277.
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
XX WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-IB01903.
XX
XX PR 28-JUL-2000; 2000US-221607P.
XX
XX PR 02-MAY-2001; 2001US-287724P.
XX
XX PA (COMP-) COMPUGEN INC.
XX
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX DR WPI; 2002-257383/30.
XX
XX PT New oligonucleotide libraries comprising oligonucleotides which
XX PT selectively hybridize to mRNAs transcribed from a transcription unit of
XX PT a genome, useful for detecting tissue-, pathology-, and
XX PT developmental-specific genes
XX
XX PS Example 1; SEQ ID 14277; 47pp; English.
XX
XX CC The present invention describes oligonucleotide libraries for detecting
XX CC messenger RNAs that populate a (sub-)transcriptome, where the
XX CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX CC transcription units that populate a genome. The library comprises
XX CC several oligonucleotides, each capable of hybridising selectively to a
XX CC set of messenger RNAs transcribed from a given transcription unit of
XX CC the genome, which encodes one or more messenger RNA splice variants.
XX CC The oligonucleotide libraries are useful for detecting mRNAs from a
XX CC biological sample, in expression profiling studies, in qualitatively or
XX CC quantitatively characterising the corresponding transcriptome, and in
XX CC detecting RNA transcripts and splice variants of human or animal
XX CC transcriptomes. The libraries may also be used as specialised mini
XX CC libraries to detect transcripts of a sub-transcriptome under a
XX CC particular biological or pathological state, and so allowing the
XX CC detection of tissue- and pathology-specific genes such as those genes
XX CC only expressed in specific tissue under a specific pathological
XX CC condition; to detect developmental specific genes; and to detect RNA
XX CC transcripts and splice variants of a transcriptome of a patient suffering
XX CC from a particular disorder. ABN27253 to ABN59589 represent
XX CC oligonucleotide sequences from rats, humans and mice, which are used in
XX CC the exemplification of the present invention.
XX CC N.B. The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pat_sequences.
XX
XX SQ Sequence 60 BP; 17 A; 12 C; 15 G; 16 T; 0 other;
XX
Query Match 66.7%; Score 14; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GATTCTAGGAATT 15
DB 52 GATTCTAGGAATT 39

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RESULT 34
ABN41529/c
ID ABN41529 standard; DNA; 60 BP.
XX
AC ABN41529;
XX
XX
XX DT 15-JUL-2002 (first entry)
XX

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```

RESULT 35
AAT58221/c
ID AAT58221 standard; DNA; 30 BP.
XX
AC AAT58221;
XX
XX
XX DT 20-MAY-1997 (first entry)
XX

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```

DE  Candida CYB1 gene primer.
XX
XX  TYPI; CYS1; CDK1; CYB1; MOC1; CMK1; cell-cycle regulatory protein;
KW  Candida; anti-mycotic; antifungal; preservative; yeast;
KW  cyclin; kinase; phosphatase; ss.
XX
OS  Synthetic.
XX
XX  WO9639527-A1.
XX
XX  12-DEC-1996.
XX
XX  05-JUN-1996; 96WO-US08807.
XX
XX  05-JUN-1995; 95US-0463090.
XX
XX  (MITO-) MITOTIX INC.
XX
XX  Cottarel G, Damagnez V, Draetta G;
XX
XX  WPI; 1997-043149/04.
XX
XX  New cell-cycle regulatory proteins from Candida - useful
XX  as anti-mycotic agents, as a preservative or in reagents and assays.
XX
XX  Example 7; Page 37; 70pp; English.
XX
XX  Six Candida genes have been isolated, which encode an apparent
XX  CDC35 phosphatase (TYPI), a p13suc1 homolog (CYS1), a cyclin
XX  dependent kinase (CDK1), a cyclin (CYB1), a CDK-activating kinase
XX  catalytic subunit (MOC1), and a Map kinase (CMK1) (AA164446 to
XX  AA164451). The TYPI polypeptide and nucleic acid is claimed, where
XX  TYPI is at least 75% homologous to the amino acid sequence given
XX  in Seq 2, according to the claims of the specification. According
XX  to the disclosure, Seq 2 encodes CYS1 (AA164446) and Seq 1 encodes
XX  TYPI (AA164447).
XX
XX  The products may be used in reagents and assays which permit the
XX  rapid detection and evaluation of Candida yeast infections and for
XX  identifying cpsds. which have antifungal properties and which may be
XX  used as anti-mycotic agents. Such agents can be used therapeutically,
XX  as well as, for example, preservatives in foodstuff, feed supplement
XX  for promoting weight gain in livestock, or in disinfectant
XX  formulations for treatment of non-living matter, e.g. for
XX  decontaminating hospital equipment and rooms.
XX
XX  Sequence 30 BP; 10 A; 6 C; 4 G; 10 T; 0 other;
XX
XX  Query Match 65.7%; Score 13.8; DB 18; Length 30;
XX  Best Local Similarity 88.2%; Pred. No. 6.1e+03;
XX  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX  3 ATTCTAGGAATTCAAA 19
XX  20 ATTACTATGATTCAAA 4
XX
XX  Db
XX
XX  RESULT 36
XX  AAV04870/c
XX  AAV04870 standard; DNA; 30 BP.
XX
XX  AAV04870;
XX
XX  30-APR-1998 (first entry)
XX
XX  PCR primer 2 used to amplify the PTPase domain of GLEPPI.
XX
XX  Glomerular epithelial protein 1; GLEPPI; podocyte; gene therapy;
XX  fibronectin type III-like repeat; protein tyrosine phosphatase domain;
XX  PTPase domain; glomerular disorder; low level; GLEPPI expression;
XX  PCR primer; ss.
XX
XX  Synthetic.
XX
XX  OS
XX

```

```

PN  US5705623-A.
XX
XX  06-JAN-1998.
XX
XX  25-FEB-1994; 94US-0201697.
XX
XX  25-FEB-1994; 94US-0201697.
XX
XX  (UNMT ) UNIV MICHIGAN.
XX
XX  Thomas PE, Wiggins RC;
XX
XX  WPI; 1998-086195/08.
XX
XX  DNA encoding glomerular epithelial protein 1 - useful for gene
XX  therapy of glomerular disorders
XX
XX  Example 3; Column 14; 47pp; English.
XX
XX  PCR primers AAV04869-70 were used to amplify the glomerular epithelial
XX  protein 1 (GLEPPI) protein tyrosine phosphatase (PTPase) segment.
XX  The PCR product was cloned to produce a fusion protein, which was tested
XX  to confirm that the PTPase domain of GLEPPI had PTPase activity.
XX  The GLEPPI protein is primarily expressed in mammalian podocytes.
XX  The protein has a large extracellular domain with a sequence containing
XX  8 fibronectin type III-like repeats, a hydrophobic transmembrane segment
XX  and a single intracellular protein tyrosine phosphatase (PTPase) domain.
XX  The GLEPPI nucleic acids are used for gene therapy of glomerular
XX  disorders associated with abnormally low levels of GLEPPI expression.
XX
XX  Sequence 30 BP; 7 A; 6 C; 4 G; 13 T; 0 other;
XX
XX  Query Match 65.7%; Score 13.8; DB 19; Length 30;
XX  Best Local Similarity 88.2%; Pred. No. 6.1e+03;
XX  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX  3 ATTCTAGGAATTCAAA 19
XX  17 AGTCTTAGGAATTCAAA 1
XX
XX  Db
XX
XX  RESULT 37
XX  AAZ08279/c
XX  AAZ08279 standard; DNA; 30 BP.
XX
XX  AAZ08279;
XX
XX  07-FEB-2000 (first entry)
XX
XX  PCR primer-1 used for amplification of Candida CYB1 gene.
XX
XX  Cell cycle regulatory protein; CYB1 gene; Candida; coding sequence;
XX  EcoRI; restriction site; primer; amplify; subclone; pUC4-5 vector;
XX  CYB1-VP16 fusion protein; ss.
XX
XX  Synthetic.
XX
XX  OS
XX
XX  WO957536-A2.
XX
XX  11-NOV-1999.
XX
XX  05-MAY-1999; 99WO-US09878.
XX
XX  05-MAY-1998; 98US-0072994.
XX
XX  (MITO-) MITOTIX INC.
XX
XX  Berlin V, Cottarel G, Damagnez V, Rudolph J, Sullivan D;
XX
XX  WPI; 2000-038847/03.
XX
XX  New Candida cyclin activated kinase 1, useful for generating vaccines
XX  and screening for its inhibitors -
XX

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```
XX Example 7; Page 60; 109pp; English.
PS
XX
CC The present DNA sequence is the PCR primer-1, that has the EcoRI
CC restriction site. It is used to amplify the Candida CYP1 coding sequence
CC and is subcloned into pUG4-5 vector to create a CYP1-VPL6 fusion protein.
XX
SQ Sequence 30 BP; 10 A; 6 C; 4 G; 10 T; 0 other;

Query Match      65.7%; Score 13.8; DB 21; Length 30;
Best Local Similarity 88.2%; Pred. No. 6.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAA 19
Db 20 ATTACTATGAAATTCAA 4

RESULT 38
ABN47639
ID ABN47639 standard; DNA; 60 BP.
XX
AC ABN47639;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:20387.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PE 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 20387; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
```

```
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 13 A; 8 C; 21 G; 18 T; 0 other;

Query Match      65.7%; Score 13.8; DB 24; Length 60;
Best Local Similarity 88.2%; Pred. No. 6.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCA 17
Db 33 AGCTTCTGGAATTCA 49

RESULT 39
ABN57384/C
ID ABN57384 standard; DNA; 65 BP.
XX
AC ABN57384;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:30132.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PE 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 30132; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
```

Search completed: February 4, 2004, 16:13:45  
Job time : 147.318 secs

CC from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC the exemplification of the present invention.  
CC N.B. The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 65 BP; 22 A; 19 C; 11 G; 13 T; 0 other;

Query Match 65.7%; Score 13.8; DB 24; Length 65;  
Best Local Similarity 88.2%; Pred. No. 6.3e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 TTCTAGGAAATTCGAATC 21  
Db 62 TTCTAGGAAATTCGAATC 46

RESULT 40  
AAQ32872/c  
ID AAQ32872 standard; DNA; 22 BP.

XX AAQ32872;

XX 29-APR-1993 (first entry)

XX Human apolipoprotein exon 4 plus-strand primer #2.

XX anchored polymerase chain reaction; APCR; apoE; mismatch;

XX epsilon 2; epsilon 4; epsilon 5; epsilon 7; ss.

XX Synthetic.

XX JF04320700-A.

XX 11-NOV-1992.

XX 17-APR-1991; 91JP-0112435.

XX 17-APR-1991; 91JP-0112435.

XX (NNTR ) NIPPON SHUJI KK.

XX WPI; 1992-426692/52.

XX Testing apolipoprotein E genotype - using polymerase chain

XX reaction primers and labelled allele-specific oligonucleotide

XX probe for hybridisation to amplified deoxyribonucleic acid

XX Claim 4; Page 11; 16pp; Japanese.

XX Primer #2 corresponds to nucleotides 5'-3618-3639-3' of ApoE. This

XX plus-strand primer is used with minus strand primer #4

XX (3'-4220-4241-5', see AAQ32874) to amplify exon 4 of the human

XX apolipoprotein gene. The epsilon 2, 4 and 7 mismatch mutations occur

XX in this region, at positions 3883, 3745 and 4141 and 4144,

XX respectively. Three sets of four oligonucleotide probes were prepared

XX to distinguish the wild-type from the mutant base at the mismatch

XX position for both the plus and the minus strands. The probe sets

XX are AAQ32875-6 and AAQ32883-4 for epsilon 2, AAQ32877-8 and AAQ32885-6

XX for epsilon 4 and AAQ32881-2 and AAQ32889-90 for epsilon 7.

XX Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 other;

Query Match 64.8%; Score 13.6; DB 13; Length 22;

Best Local Similarity 80.0%; Pred. No. 7.4e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GATTCTAGGAAATTCGAATC 21  
Db 21 GATTCTAGGAAATTCGAATC 2

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 16:50:14 ; Search time 131.409 Seconds  
(without alignments)  
588.668 Million cell updates/sec

Title: US-09-744-875A-1

Perfect score: 21

Sequence: 1 agattctcagaatccaatc 21

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues 1515108

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published Applications NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	18	85.7	20 11	US-09-954-987B-30
2	18	85.7	21 11	US-09-877-705A-91
3	18	85.7	21 11	US-09-877-705A-92
4	18	85.7	21 11	US-09-877-738A-91
5	18	85.7	21 11	US-09-877-738A-92
6	18	85.7	21 11	US-09-877-738A-91
7	18	85.7	21 11	US-09-877-738A-92
8	18	85.7	21 11	US-09-877-738A-91
9	18	85.7	21 11	US-09-877-738A-92
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11	18	85.7	21 11	US-09-877-738A-92
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15	18	85.7	21 11	US-09-877-738A-92
16	18	85.7	21 11	US-09-877-738A-91
17	18	85.7	21 11	US-09-877-738A-92
18	18	85.7	21 11	US-09-877-738A-91

16	18	85.7	100 13	US-10-351-157-44	Sequence 44, Appl
17	18	85.7	100 13	US-10-351-157-45	Sequence 45, Appl
18	18	85.7	100 13	US-10-295-723-59	Sequence 59, Appl
19	18	85.7	100 15	US-10-295-723-60	Sequence 60, Appl
20	15.4	73.3	24 13	US-10-325-606-1	Sequence 1, Appl
21	14.8	70.5	41 12	US-10-327-481A-21	Sequence 21, Appl
22	14.8	70.5	41 12	US-10-327-481A-23	Sequence 23, Appl
23	14.8	70.5	44 12	US-10-327-481A-19	Sequence 19, Appl
24	14.8	70.5	44 12	US-10-327-481A-25	Sequence 25, Appl
25	14.6	69.5	58 9	US-09-932-679-42	Sequence 42, Appl
26	14.6	69.5	58 13	US-09-969-723-46	Sequence 46, Appl
27	14.2	67.6	99 10	US-09-969-723-1158	Sequence 1158, Ap
28	14	66.7	60 13	US-09-908-975-14277	Sequence 14277, A
29	13.8	65.7	20 11	US-09-920-073-115	Sequence 115, App
30	13.8	65.7	20 12	US-10-388-263-651	Sequence 651, App
31	13.8	65.7	20 13	US-10-147-156-115	Sequence 115, App
32	13.8	65.7	60 13	US-09-908-975-20387	Sequence 20387, A
33	13.8	65.7	65 13	US-09-908-975-30132	Sequence 30132, A
34	13.6	64.8	25 15	US-10-098-263B-26232	Sequence 26232, A
35	13.6	64.8	44 13	US-10-307-441-42	Sequence 42, Appl
36	13.4	63.8	28 12	US-09-927-876-69	Sequence 69, Appl
37	13.4	63.8	28 13	US-10-360-149-69	Sequence 69, Appl
38	13.4	63.8	65 13	US-09-908-975-28326	Sequence 28326, A
39	13.2	62.9	19 13	US-10-251-117-633	Sequence 633, App
40	13.2	62.9	19 13	US-10-251-117-940	Sequence 940, App
41	13.2	62.9	25 15	US-10-098-263B-107625	Sequence 107625, i
42	13.2	62.9	42 13	US-10-154-460-2	Sequence 2, Appli
43	13.2	62.9	43 13	US-10-032-585-811	Sequence 811, App
44	13.2	62.9	50 12	US-10-131-827-8112	Sequence 8112, App
45	13.2	62.9	60 13	US-09-908-975-16848	Sequence 16848, A
46	13.2	62.9	60 13	US-09-737-476B-39	Sequence 39, Appl
47	13.2	62.9	63 13	US-10-197-293-38	Sequence 38, Appl
48	13.2	62.9	65 13	US-10-032-585-2560	Sequence 2560, Ap
49	13	61.9	22 10	US-09-881-012-130	Sequence 12, Appl
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51	13	61.9	25 15	US-10-098-263B-42396	Sequence 42396, A
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53	13	61.9	25 15	US-10-098-263B-117738	Sequence 117738, A
54	13	61.9	26 12	US-10-024-212-404	Sequence 404, App
55	13	61.9	26 12	US-10-024-212-407	Sequence 407, App
56	13	61.9	26 12	US-10-024-212-410	Sequence 410, App
57	13	61.9	26 12	US-10-024-212-413	Sequence 413, App
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59	13	61.9	27 13	US-10-271-012-15	Sequence 15, Appl
60	13	61.9	27 15	US-10-011-366-15	Sequence 15, Appl
61	13	61.9	30 10	US-09-927-933A-14	Sequence 14, Appl
62	13	61.9	30 10	US-09-927-933A-15	Sequence 15, Appl
63	13	61.9	35 13	US-10-364-276-2	Sequence 2, Appli
64	13	61.9	41 13	US-10-071-302-31	Sequence 31, Appl
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66	13	61.9	50 10	US-09-832-659-30	Sequence 30, Appl
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68	13	61.9	50 12	US-10-131-827-2207	Sequence 2207, Ap
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74	12.8	61.0	32 15	US-10-071-485-54	Sequence 54, Appl
75	12.8	61.0	33 9	US-09-863-179-2	Sequence 2, Appli
76	12.8	61.0	34 13	US-10-339-740-188	Sequence 188, App
77	12.8	61.0	36 13	US-10-210-023-61	Sequence 61, Appl
78	12.8	61.0	37 15	US-10-234-339-10	Sequence 10, Appl
79	12.8	61.0	43 11	US-09-507-362-38	Sequence 38, Appl
80	12.8	61.0	43 12	US-10-346-880-88	Sequence 88, Appl
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82	12.8	61.0	50 12	US-10-391-441-38	Sequence 38, Appl
83	12.8	61.0	53 12	US-10-131-827-4046	Sequence 4046, Ap
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86	12.8	61.0	61 11	US-09-907-111-80	Sequence 80, Appl
87	12.8	61.0	61 11	US-09-907-111-82	Sequence 82, Appl
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C 89	12.8	61.0	65	13	US-10-032-585-2193	Sequence 2193, Ap	162	12.2	58.1	24	10	US-09-993-687-190	Sequence 190, App
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C 91	12.6	60.0	24	15	US-08-834-705-63	Sequence 63, Appl	164	12.2	58.1	24	11	US-09-997-653-190	Sequence 190, App
C 92	12.6	60.0	25	15	US-10-098-2638-27569	Sequence 27569, A	165	12.2	58.1	24	11	US-09-993-667-190	Sequence 190, App
C 93	12.6	60.0	25	15	US-10-098-2638-58686	Sequence 58686, A	166	12.2	58.1	24	11	US-09-997-628-190	Sequence 190, App
C 94	12.6	60.0	25	15	US-10-098-2638-110960	Sequence 110960, A	167	12.2	58.1	24	11	US-09-997-666-190	Sequence 190, App
C 95	12.6	60.0	25	15	US-10-098-2638-115527	Sequence 115527, A	168	12.2	58.1	24	11	US-09-990-438-190	Sequence 190, App
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C 97	12.6	60.0	27	13	US-10-183-770-33	Sequence 33, Appl	170	12.2	58.1	24	11	US-09-990-711-190	Sequence 190, App
C 98	12.6	60.0	27	13	US-10-254-905-75	Sequence 75, Appl	171	12.2	58.1	24	11	US-09-989-726-190	Sequence 190, App
C 99	12.6	60.0	27	13	US-10-395-812-21	Sequence 21, Appl	172	12.2	58.1	24	11	US-09-989-156-190	Sequence 190, App
C 100	12.6	60.0	27	15	US-10-071-458-27	Sequence 27, Appl	173	12.2	58.1	24	11	US-09-990-437-190	Sequence 190, App
C 101	12.6	60.0	36	13	US-09-843-905A-10	Sequence 10, Appl	174	12.2	58.1	24	11	US-09-991-157-190	Sequence 190, App
C 102	12.6	60.0	37	10	US-09-843-905A-10	Sequence 10, Appl	175	12.2	58.1	24	11	US-09-997-573-190	Sequence 190, App
C 103	12.6	60.0	37	13	US-10-317-250-10	Sequence 10, Appl	176	12.2	58.1	24	11	US-09-991-172-190	Sequence 190, App
C 104	12.6	60.0	39	15	US-10-005-956-1360	Sequence 1360, Ap	177	12.2	58.1	24	11	US-09-990-126-190	Sequence 190, App
C 105	12.6	60.0	39	15	US-10-005-956-1494	Sequence 1494, Ap	178	12.2	58.1	24	11	US-09-997-559-190	Sequence 190, App
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C 107	12.6	60.0	60	13	US-09-908-975-18505	Sequence 18505, A	180	12.2	58.1	24	11	US-09-990-443-190	Sequence 190, App
C 108	12.6	60.0	60	13	US-09-908-975-20819	Sequence 20819, A	181	12.2	58.1	24	11	US-09-991-854-190	Sequence 190, App
C 109	12.6	60.0	60	13	US-09-908-975-22479	Sequence 22479, A	182	12.2	58.1	24	11	US-09-997-628-190	Sequence 190, App
C 110	12.6	60.0	65	13	US-10-032-585-504	Sequence 504, App	183	12.2	58.1	24	11	US-09-997-683-190	Sequence 190, App
C 111	12.6	60.0	65	13	US-10-032-585-504	Sequence 504, App	184	12.2	58.1	24	11	US-09-997-683-190	Sequence 190, App
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C 118	12.6	60.0	79	13	US-10-329-465-259	Sequence 259, App	191	12.2	58.1	24	11	US-09-997-748-190	Sequence 190, App
C 119	12.6	60.0	80	9	US-09-157-748-43	Sequence 43, Appl	192	12.2	58.1	24	11	US-09-990-439-190	Sequence 190, App
C 120	12.6	60.0	98	10	US-09-878-574-15211	Sequence 15211, A	193	12.2	58.1	24	11	US-09-990-427-190	Sequence 190, App
C 121	12.4	59.0	20	10	US-09-813-824A-25	Sequence 25, Appl	194	12.2	58.1	24	11	US-09-989-828-190	Sequence 190, App
C 122	12.4	59.0	20	10	US-09-813-824A-25	Sequence 25, Appl	195	12.2	58.1	24	11	US-09-993-583-190	Sequence 190, App
C 123	12.4	59.0	20	13	US-10-171-319-38	Sequence 38, Appl	196	12.2	58.1	24	11	US-09-941-992-190	Sequence 190, App
C 124	12.4	59.0	21	12	US-10-171-319-43	Sequence 43, Appl	197	12.2	58.1	24	11	US-09-992-521-190	Sequence 190, App
C 125	12.4	59.0	21	12	US-10-349-143-10711	Sequence 10711, A	198	12.2	58.1	24	11	US-09-997-333-190	Sequence 190, App
C 126	12.4	59.0	23	11	US-09-981-803-34	Sequence 34, Appl	199	12.2	58.1	24	11	US-09-997-384-190	Sequence 190, App
C 127	12.4	59.0	25	15	US-10-098-2638-107825	Sequence 107825, A	200	12.2	58.1	24	11	US-09-998-041-190	Sequence 190, App
C 128	12.4	59.0	25	15	US-10-098-2638-107826	Sequence 107826, A	201	12.2	58.1	24	11	US-09-997-185-190	Sequence 190, App
C 129	12.4	59.0	28	9	US-09-921-068-4	Sequence 4, Appl1	202	12.2	58.1	24	11	US-09-997-614-190	Sequence 190, App
C 130	12.4	59.0	30	9	US-09-475-674-18	Sequence 18, Appl1	203	12.2	58.1	24	12	US-09-989-733-190	Sequence 190, App
C 131	12.4	59.0	30	15	US-10-080-713-18	Sequence 18, Appl	204	12.2	58.1	24	12	US-09-992-643-190	Sequence 190, App
C 132	12.4	59.0	37	9	US-09-737-178-140	Sequence 140, App	205	12.2	58.1	24	13	US-09-989-862-190	Sequence 190, App
C 133	12.4	59.0	37	11	US-09-853-079-140	Sequence 140, App	206	12.2	58.1	24	13	US-09-989-725-190	Sequence 190, App
C 134	12.4	59.0	47	12	US-10-349-143-3822	Sequence 322, App	207	12.2	58.1	24	13	US-09-997-529-190	Sequence 190, App
C 135	12.4	59.0	50	12	US-10-131-827-8852	Sequence 8852, App	208	12.2	58.1	24	13	US-10-219-538-190	Sequence 190, App
C 136	12.4	59.0	65	13	US-09-908-975-18238	Sequence 18238, A	209	12.2	58.1	24	14	US-10-076-900-14	Sequence 14, Appl
C 137	12.4	59.0	65	13	US-09-908-975-25462	Sequence 25462, A	210	12.2	58.1	24	15	US-10-098-2638-8302	Sequence 8302, Ap
C 138	12.4	59.0	87	13	US-09-783-590-2523	Sequence 2523, Ap	211	12.2	58.1	25	15	US-10-098-2638-58303	Sequence 58303, A
C 139	12.4	59.0	87	13	US-10-029-386-21389	Sequence 21389, Ap	212	12.2	58.1	25	15	US-10-098-2638-78946	Sequence 78946, A
C 140	12.2	58.1	17	11	US-09-848-754A-1157	Sequence 1157, Ap	213	12.2	58.1	25	15	US-10-098-2638-99687	Sequence 99687, A
C 141	12.2	58.1	20	11	US-09-953-611-59	Sequence 59, Appl1	214	12.2	58.1	26	15	US-10-098-2638-114433	Sequence 114433, A
C 142	12.2	58.1	21	12	US-10-349-143-8328	Sequence 8328, Ap	215	12.2	58.1	26	15	US-09-887-593-17	Sequence 17, Appl1
C 143	12.2	58.1	24	9	US-09-989-722-190	Sequence 190, App	216	12.2	58.1	27	12	US-10-317-444-413	Sequence 413, App
C 144	12.2	58.1	24	9	US-09-989-722-190	Sequence 190, App	217	12.2	58.1	27	12	US-10-317-444-414	Sequence 414, App
C 145	12.2	58.1	24	9	US-09-989-729-190	Sequence 190, App	218	12.2	58.1	27	12	US-10-317-444-415	Sequence 415, App
C 146	12.2	58.1	24	9	US-09-989-727-190	Sequence 190, App	219	12.2	58.1	27	12	US-10-317-444-416	Sequence 416, App
C 147	12.2	58.1	24	9	US-09-989-731-190	Sequence 190, App	220	12.2	58.1	28	13	US-10-440-066-16	Sequence 16, Appl
C 148	12.2	58.1	24	10	US-09-989-732-190	Sequence 190, App	221	12.2	58.1	30	11	US-09-907-111-196	Sequence 166, Appl
C 149	12.2	58.1	24	10	US-09-991-073-190	Sequence 190, App	222	12.2	58.1	30	13	US-10-104-019-99	Sequence 99, Appl
C 150	12.2	58.1	24	10	US-09-990-442-190	Sequence 190, App	223	12.2	58.1	30	13	US-10-428-826-51	Sequence 51, Appl
C 151	12.2	58.1	24	10	US-09-991-163-190	Sequence 190, App	224	12.2	58.1	30	14	US-10-104-019-99	Sequence 99, Appl
C 152	12.2	58.1	24	10	US-09-993-604-190	Sequence 190, App	225	12.2	58.1	36	15	US-10-054-965-10	Sequence 10, Appl
C 153	12.2	58.1	24	10	US-09-990-456-190	Sequence 190, App	226	12.2	58.1	36	15	US-10-257-477-6	Sequence 6, Appl1
C 154	12.2	58.1	24	10	US-09-989-721-190	Sequence 190, App	227	12.2	58.1	43	13	US-10-001-886B-3	Sequence 3, Appl1
C 155	12.2	58.1	24	10	US-09-992-598-190	Sequence 190, App	228	12.2	58.1	47	13	US-10-367-438-54	Sequence 54, Appl
C 156	12.2	58.1	24	10	US-09-989-293A-190	Sequence 190, App	229	12.2	58.1	49	15	US-10-287-919-452	Sequence 452, App
C 157	12.2	58.1	24	10	US-09-989-735-190	Sequence 190, App	230	12.2	58.1	52	9	US-09-777-564A-1717	Sequence 1717, Ap
C 158	12.2	58.1	24	10	US-09-990-444-190	Sequence 190, App	231	12.2	58.1	52	15	US-10-015-219-1717	Sequence 1717, Ap
C 159	12.2	58.1	24	10	US-09-991-181-190	Sequence 190, App	232	12.2	58.1	58	11	US-09-907-111-235	Sequence 235, App
C 160	12.2	58.1	24	10	US-09-989-730-190	Sequence 190, App	233	12.2	58.1	58	11	US-09-907-111-235	Sequence 235, App
C 161	12.2	58.1	24	10	US-09-990-436-190	Sequence 190, App	234	12.2	58.1	58	11	US-09-907-111-238	Sequence 238, App



C 235	12.2	58.1	60	13	US-09-908-975-10544	Sequence 10544, A	C 308	12	57.1	65	13	US-09-908-975-27340	Sequence 27340, A
C 236	12.2	58.1	60	13	US-09-908-975-22035	Sequence 22035, A	C 309	12	57.1	65	13	US-09-908-975-27340	Sequence 27340, A
C 237	12.2	58.1	60	14	US-10-006-611-5	Sequence 5, Appli	C 310	12	57.1	65	13	US-09-908-975-27891	Sequence 27891, A
C 238	12.2	58.1	61	11	US-09-907-111-58	Sequence 48, Appli	C 311	12	57.1	65	13	US-09-908-975-29085	Sequence 29085, A
C 239	12.2	58.1	61	15	US-10-205-009-48	Sequence 440, A	C 312	12	57.1	65	13	US-10-032-585-1520	Sequence 2729, Ap
C 240	12.2	58.1	65	13	US-09-908-975-25014	Sequence 25014, A	C 313	12	57.1	65	13	US-10-032-585-2729	Sequence 2829, Ap
C 241	12.2	58.1	65	13	US-10-032-585-440	Sequence 2546, Ap	C 314	12	57.1	71	11	US-09-940-925A-164	Sequence 164, App
C 242	12.2	58.1	65	13	US-10-032-585-2546	Sequence 3918, Ap	C 315	12	57.1	71	11	US-09-941-193A-164	Sequence 164, App
C 243	12.2	58.1	65	13	US-10-023-386-17285	Sequence 17285, A	C 316	12	57.1	84	15	US-09-941-193A-164	Sequence 164, App
C 244	12.2	58.1	77	13	US-10-023-386-21454	Sequence 21454, A	C 317	12	57.1	84	15	US-09-941-193A-164	Sequence 164, App
C 245	12.2	58.1	89	13	US-10-023-386-22503	Sequence 22503, A	C 318	12	57.1	84	15	US-09-941-193A-164	Sequence 164, App
C 246	12.2	58.1	91	13	US-09-818-875-967	Sequence 967, App	C 319	12	57.1	89	9	US-09-854-761-2473	Sequence 2473, A
C 247	12	57.1	17	11	US-09-818-875-968	Sequence 968, App	C 320	12	57.1	89	9	US-09-854-761-2473	Sequence 2473, A
C 248	12	57.1	17	11	US-10-261-185-967	Sequence 967, App	C 321	12	57.1	93	13	US-10-287-806-18	Sequence 18, Appli
C 249	12	57.1	17	12	US-10-261-185-967	Sequence 968, App	C 322	12	57.1	96	9	US-09-864-761-31003	Sequence 31003, A
C 250	12	57.1	17	12	US-10-261-185-968	Sequence 968, App	C 323	12	57.1	98	9	US-09-777-564-865	Sequence 865, App
C 251	12	57.1	17	13	US-10-209-787-967	Sequence 967, App	C 324	12	57.1	98	15	US-10-015-219-865	Sequence 865, App
C 252	12	57.1	17	13	US-10-209-787-968	Sequence 968, App	C 325	12	57.1	100	12	US-10-242-535A-20804	Sequence 20804, A
C 253	12	57.1	20	11	US-09-784-674-596	Sequence 596, App	C 326	12	56.2	15	13	US-10-440-850-850	Sequence 850, App
C 254	12	57.1	21	13	US-10-353-454-46	Sequence 46, Appli	C 327	11.8	56.2	17	11	US-09-730-289B-630	Sequence 630, App
C 255	12	57.1	24	9	US-09-759-960-13	Sequence 13, Appli	C 328	11.8	56.2	17	11	US-09-740-332-2559	Sequence 2559, Ap
C 256	12	57.1	24	9	US-09-759-960-15	Sequence 15, Appli	C 329	11.8	56.2	17	11	US-09-817-879-2559	Sequence 2559, Ap
C 257	12	57.1	25	9	US-09-866-108-13727	Sequence 13727, A	C 330	11.8	56.2	17	15	US-10-156-306-349	Sequence 349, App
C 258	12	57.1	25	9	US-09-866-108-13728	Sequence 13728, A	C 331	11.8	56.2	17	15	US-10-156-306-349	Sequence 3702, Ap
C 259	12	57.1	25	9	US-09-866-108-13729	Sequence 13729, A	C 332	11.8	56.2	20	13	US-09-179-536B-79	Sequence 79, Appli
C 260	12	57.1	25	9	US-09-866-108-13730	Sequence 13730, A	C 333	11.8	56.2	21	9	US-09-402-576A-79	Sequence 48, Appli
C 261	12	57.1	25	9	US-09-866-108-13731	Sequence 13731, A	C 334	11.8	56.2	25	10	US-09-932-058-1	Sequence 1, Appli
C 262	12	57.1	25	9	US-09-839-894-23	Sequence 23, Appli	C 335	11.8	56.2	25	10	US-09-932-058-2	Sequence 2, Appli
C 263	12	57.1	25	9	US-09-866-108-13732	Sequence 13732, A	C 336	11.8	56.2	25	10	US-09-932-058-4	Sequence 4, Appli
C 264	12	57.1	25	15	US-10-098-263B-26231	Sequence 26231, A	C 337	11.8	56.2	25	13	US-10-449-456-9	Sequence 9, Appli
C 265	12	57.1	25	15	US-10-098-263B-67057	Sequence 67057, A	C 338	11.8	56.2	25	13	US-10-449-456-4	Sequence 4044, Ap
C 266	12	57.1	25	15	US-10-098-263B-68789	Sequence 68789, A	C 339	11.8	56.2	25	15	US-10-098-263B-82245	Sequence 82245, A
C 267	12	57.1	29	10	US-09-742-361A-3	Sequence 3, Appli	C 340	11.8	56.2	25	15	US-10-098-263B-82829	Sequence 32829, A
C 268	12	57.1	29	11	US-09-894-912A-44	Sequence 44, Appli	C 341	11.8	56.2	25	15	US-10-098-263B-84510	Sequence 84510, A
C 269	12	57.1	29	13	US-10-071-962-4	Sequence 4, Appli	C 342	11.8	56.2	25	15	US-10-098-263B-89230	Sequence 89230, A
C 270	12	57.1	30	10	US-09-985-157-5	Sequence 5, Appli	C 343	11.8	56.2	25	15	US-10-098-263B-107397	Sequence 107397, A
C 271	12	57.1	30	11	US-09-853-079-157	Sequence 157, App	C 344	11.8	56.2	25	15	US-10-098-263B-111157	Sequence 111157, A
C 272	12	57.1	30	13	US-10-002-244-29	Sequence 29, Appli	C 345	11.8	56.2	28	7	US-08-462-386B-39	Sequence 39, Appli
C 273	12	57.1	30	13	US-10-246-229-6	Sequence 6, Appli	C 346	11.8	56.2	28	8	US-08-954-771-39	Sequence 39, Appli
C 274	12	57.1	30	15	US-10-044-967-5	Sequence 29, Appli	C 347	11.8	56.2	28	10	US-09-863-339-10	Sequence 10, Appli
C 275	12	57.1	30	15	US-10-044-967-5	Sequence 5, Appli	C 348	11.8	56.2	28	13	US-09-736-676-16	Sequence 39, Appli
C 276	12	57.1	31	1	US-09-841-132-216	Sequence 216, App	C 349	11.8	56.2	29	13	US-10-449-456-16	Sequence 16, Appli
C 277	12	57.1	31	11	US-09-848-616-9	Sequence 9, Appli	C 350	11.8	56.2	30	9	US-09-792-420-4	Sequence 4, Appli
C 278	12	57.1	31	13	US-10-050-902-9	Sequence 9, Appli	C 351	11.8	56.2	30	15	US-10-251-385-102	Sequence 102, App
C 279	12	57.1	31	13	US-10-050-902-9	Sequence 9, Appli	C 352	11.8	56.2	31	9	US-09-801-274-52	Sequence 52, Appli
C 280	12	57.1	33	12	US-10-387-384-22	Sequence 22, Appli	C 353	11.8	56.2	31	15	US-10-093-037-32	Sequence 32, Appli
C 281	12	57.1	33	13	US-09-731-030A-7	Sequence 4, Appli	C 354	11.8	56.2	33	14	US-10-136-139-2	Sequence 2, Appli
C 282	12	57.1	37	10	US-09-944-411-11	Sequence 11, Appli	C 355	11.8	56.2	33	15	US-09-924-366A-1	Sequence 6, Appli
C 283	12	57.1	38	10	US-09-759-352-3	Sequence 3, Appli	C 356	11.8	56.2	33	15	US-09-981-886A-13	Sequence 13, Appli
C 284	12	57.1	38	10	US-10-260-516-11	Sequence 11, Appli	C 357	11.8	56.2	43	13	US-10-280-137-187	Sequence 187, App
C 285	12	57.1	38	13	US-10-220-612-9	Sequence 20, Appli	C 358	11.8	56.2	43	13	US-09-832-659-11	Sequence 11, Appli
C 286	12	57.1	39	13	US-09-826-509-20	Sequence 841, App	C 359	11.8	56.2	47	10	US-09-832-659-31	Sequence 31, Appli
C 287	12	57.1	43	13	US-10-032-585-841	Sequence 734, App	C 360	11.8	56.2	47	12	US-10-170-097-829	Sequence 829, App
C 288	12	57.1	50	12	US-10-131-827-734	Sequence 5800, App	C 361	11.8	56.2	47	12	US-10-349-413-1257	Sequence 1257, App
C 289	12	57.1	50	12	US-10-131-827-5919	Sequence 5919, App	C 362	11.8	56.2	50	10	US-09-932-058-4	Sequence 4, Appli
C 290	12	57.1	50	12	US-10-131-827-7651	Sequence 7651, App	C 363	11.8	56.2	50	10	US-09-932-058-5	Sequence 5, Appli
C 291	12	57.1	51	10	US-09-828-995B-91	Sequence 91, Appli	C 364	11.8	56.2	50	10	US-09-909-920-79	Sequence 79, Appli
C 292	12	57.1	51	10	US-10-027-632-58675	Sequence 58675, A	C 365	11.8	56.2	50	10	US-09-909-920-79	Sequence 79, Appli
C 293	12	57.1	53	13	US-09-852-385-7	Sequence 7, Appli	C 366	11.8	56.2	50	10	US-09-905-291A-79	Sequence 79, Appli
C 294	12	57.1	60	11	US-09-908-975-6825	Sequence 6825, App	C 367	11.8	56.2	50	10	US-09-907-824-79	Sequence 79, Appli
C 295	12	57.1	60	13	US-09-908-975-7405	Sequence 7405, App	C 368	11.8	56.2	50	10	US-09-907-824-79	Sequence 79, Appli
C 296	12	57.1	60	13	US-09-908-975-8674	Sequence 8674, App	C 369	11.8	56.2	50	11	US-09-904-011-79	Sequence 79, Appli
C 297	12	57.1	60	13	US-09-908-975-13716	Sequence 13716, A	C 370	11.8	56.2	50	11	US-09-906-838-79	Sequence 79, Appli
C 298	12	57.1	60	13	US-09-908-975-14758	Sequence 14758, A	C 371	11.8	56.2	50	11	US-09-907-813-79	Sequence 79, Appli
C 299	12	57.1	60	13	US-09-908-975-16941	Sequence 16941, A	C 372	11.8	56.2	50	11	US-09-907-813-79	Sequence 79, Appli
C 300	12	57.1	60	13	US-09-908-975-19593	Sequence 19593, A	C 373	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli
C 301	12	57.1	60	13	US-09-908-975-20092	Sequence 20092, A	C 374	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli
C 302	12	57.1	60	13	US-09-908-975-20471	Sequence 20471, A	C 375	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli
C 303	12	57.1	60	13	US-09-908-975-20471	Sequence 20471, A	C 376	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli
C 304	12	57.1	65	13	US-09-908-975-20471	Sequence 20471, A	C 377	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli
C 305	12	57.1	65	13	US-09-908-975-20471	Sequence 20471, A	C 378	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli
C 306	12	57.1	65	13	US-09-908-975-20471	Sequence 20471, A	C 379	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli
C 307	12	57.1	65	13	US-09-908-975-20471	Sequence 20471, A	C 380	11.8	56.2	50	11	US-09-904-852-79	Sequence 79, Appli

C 381	11.8	56.2	50	11	US-09-904-786-79	Sequence 79, Appl	C 454	11.6	55.2	22	13	US-10-026-952-36	Sequence 36, Appl
C 382	11.8	56.2	50	11	US-09-906-646-79	Sequence 79, Appl	C 455	11.6	55.2	23	11	US-09-860-738C-8	Sequence 8, Appl
C 383	11.8	56.2	50	11	US-09-906-700-79	Sequence 79, Appl	C 456	11.6	55.2	23	11	US-10-291-171-16	Sequence 16, Appl
C 384	11.8	56.2	50	11	US-09-903-786-79	Sequence 79, Appl	C 457	11.6	55.2	23	15	US-10-081-980B-5	Sequence 5, Appl
C 385	11.8	56.2	50	11	US-09-902-903-79	Sequence 79, Appl	C 458	11.6	55.2	25	15	US-10-215-112-3087	Sequence 3087, Ap
C 386	11.8	56.2	50	11	US-09-903-749A-79	Sequence 79, Appl	C 459	11.6	55.2	25	15	US-10-215-112-3508	Sequence 18794, A
C 387	11.8	56.2	50	11	US-09-904-119-79	Sequence 79, Appl	C 460	11.6	55.2	25	15	US-10-098-263B-18794	Sequence 40243, A
C 388	11.8	56.2	50	11	US-09-904-958-79	Sequence 79, Appl	C 461	11.6	55.2	25	15	US-10-098-263B-44235	Sequence 44235, A
C 389	11.8	56.2	50	11	US-09-904-936-79	Sequence 79, Appl	C 462	11.6	55.2	25	15	US-10-098-263B-46762	Sequence 46762, A
C 390	11.8	56.2	50	11	US-09-907-794-79	Sequence 79, Appl	C 463	11.6	55.2	25	15	US-10-098-263B-50109	Sequence 50109, A
C 391	11.8	56.2	50	11	US-09-903-943-79	Sequence 79, Appl	C 464	11.6	55.2	25	15	US-10-098-263B-68737	Sequence 68737, A
C 392	11.8	56.2	50	11	US-09-904-462-79	Sequence 79, Appl	C 465	11.6	55.2	25	15	US-10-098-263B-68738	Sequence 68939, A
C 393	11.8	56.2	50	11	US-09-907-925-79	Sequence 79, Appl	C 466	11.6	55.2	25	15	US-10-098-263B-87751	Sequence 87751, A
C 394	11.8	56.2	50	11	US-09-902-692-79	Sequence 79, Appl	C 467	11.6	55.2	25	15	US-10-098-263B-88593	Sequence 88593, A
C 395	11.8	56.2	50	11	US-09-903-520-79	Sequence 79, Appl	C 468	11.6	55.2	25	15	US-10-098-263B-99377	Sequence 99373, A
C 396	11.8	56.2	50	11	US-09-905-056-79	Sequence 79, Appl	C 469	11.6	55.2	25	15	US-10-098-263B-107626	Sequence 107626, A
C 397	11.8	56.2	50	11	US-09-909-064-79	Sequence 79, Appl	C 470	11.6	55.2	25	15	US-10-098-263B-125202	Sequence 125202, A
C 398	11.8	56.2	50	11	US-09-904-553-79	Sequence 79, Appl	C 471	11.6	55.2	25	15	US-10-098-263B-125838	Sequence 125838, A
C 399	11.8	56.2	50	11	US-09-905-381-79	Sequence 79, Appl	C 472	11.6	55.2	27	15	US-10-062-809-68	Sequence 68, Appl
C 400	11.8	56.2	50	11	US-09-905-088-79	Sequence 79, Appl	C 473	11.6	55.2	27	15	US-10-026-952-38	Sequence 38, Appl
C 401	11.8	56.2	50	11	US-09-907-575-79	Sequence 79, Appl	C 474	11.6	55.2	28	13	US-09-801-874-1015	Sequence 1015, Ap
C 402	11.8	56.2	50	11	US-09-905-075-79	Sequence 79, Appl	C 475	11.6	55.2	31	9	US-09-844-813-6	Sequence 6, Appl
C 403	11.8	56.2	50	11	US-09-902-759-79	Sequence 79, Appl	C 476	11.6	55.2	32	9	US-09-832-893-20	Sequence 20, Appl
C 404	11.8	56.2	50	11	US-09-902-634-79	Sequence 79, Appl	C 477	11.6	55.2	33	13	US-09-828-523A-52	Sequence 52, Appl
C 405	11.8	56.2	50	11	US-09-902-713-79	Sequence 79, Appl	C 478	11.6	55.2	40	11	US-09-966-521-92	Sequence 92, Appl
C 406	11.8	56.2	50	11	US-09-907-979-79	Sequence 79, Appl	C 479	11.6	55.2	40	13	US-10-429-094-92	Sequence 92, Appl
C 407	11.8	56.2	50	11	US-09-902-615-79	Sequence 79, Appl	C 480	11.6	55.2	42	13	US-10-091-135-54	Sequence 54, Appl
C 408	11.8	56.2	50	11	US-09-903-925-79	Sequence 79, Appl	C 481	11.6	55.2	43	13	US-10-032-585-1712	Sequence 1712, Ap
C 409	11.8	56.2	50	11	US-09-906-760A-79	Sequence 79, Appl	C 482	11.6	55.2	44	12	US-09-775-925-19	Sequence 19, Appl
C 410	11.8	56.2	50	11	US-09-903-823-79	Sequence 79, Appl	C 483	11.6	55.2	47	12	US-10-349-143-690	Sequence 690, App
C 411	11.8	56.2	50	11	US-09-907-652-79	Sequence 79, Appl	C 484	11.6	55.2	47	12	US-10-349-143-1489	Sequence 1489, Ap
C 412	11.8	56.2	50	11	US-09-902-572A-79	Sequence 79, Appl	C 485	11.6	55.2	47	12	US-10-349-143-1713	Sequence 1713, Ap
C 413	11.8	56.2	50	11	US-09-902-979-79	Sequence 79, Appl	C 486	11.6	55.2	47	12	US-10-349-143-1713	Sequence 3713, Ap
C 414	11.8	56.2	50	11	US-09-905-125-79	Sequence 79, Appl	C 487	11.6	55.2	49	15	US-10-291-230-5	Sequence 5, Appl
C 415	11.8	56.2	50	11	US-09-906-815A-79	Sequence 79, Appl	C 488	11.6	55.2	49	15	US-10-291-249-5	Sequence 995, App
C 416	11.8	56.2	50	12	US-09-908-576-79	Sequence 79, Appl	C 489	11.6	55.2	50	12	US-10-131-827-995	Sequence 995, App
C 417	11.8	56.2	50	12	US-10-448-713-79	Sequence 79, Appl	C 490	11.6	55.2	50	12	US-10-131-827-1066	Sequence 1066, Ap
C 418	11.8	56.2	50	12	US-10-449-656-79	Sequence 79, Appl	C 491	11.6	55.2	50	12	US-10-131-827-1067	Sequence 1067, Ap
C 419	11.8	56.2	50	12	US-10-131-827-636	Sequence 636, App	C 492	11.6	55.2	50	12	US-10-131-827-1067	Sequence 1067, Ap
C 420	11.8	56.2	50	12	US-10-131-827-8091	Sequence 8091, Ap	C 493	11.6	55.2	50	12	US-10-131-827-1067	Sequence 1067, Ap
C 421	11.8	56.2	50	13	US-09-903-806-79	Sequence 79, Appl	C 494	11.6	55.2	52	15	US-10-062-809-60	Sequence 60, Appl
C 422	11.8	56.2	50	13	US-09-904-992-79	Sequence 79, Appl	C 495	11.6	55.2	52	15	US-09-908-975-7489	Sequence 7489, Ap
C 423	11.8	56.2	50	13	US-09-904-992-79	Sequence 79, Appl	C 496	11.6	55.2	60	13	US-09-908-975-9568	Sequence 9568, Ap
C 424	11.8	56.2	50	13	US-09-903-603A-79	Sequence 79, Appl	C 497	11.6	55.2	60	13	US-09-908-975-12289	Sequence 12289, A
C 425	11.8	56.2	50	13	US-09-904-838-79	Sequence 79, Appl	C 498	11.6	55.2	60	13	US-09-908-975-13415	Sequence 13415, A
C 426	11.8	56.2	50	13	US-09-906-1777-79	Sequence 79, Appl	C 499	11.6	55.2	60	13	US-09-908-975-14265	Sequence 14265, A
C 427	11.8	56.2	50	13	US-09-904-532-79	Sequence 79, Appl	C 500	11.6	55.2	60	13	US-09-908-975-14265	Sequence 14265, A
C 428	11.8	56.2	50	13	US-09-904-766-79	Sequence 79, Appl	C 501	11.6	55.2	60	13	US-09-908-975-17086	Sequence 17086, A
C 429	11.8	56.2	50	13	US-09-904-920A-79	Sequence 79, Appl	C 502	11.6	55.2	60	13	US-09-908-975-20914	Sequence 20914, A
C 430	11.8	56.2	50	13	US-10-299-976-79	Sequence 79, Appl	C 503	11.6	55.2	60	13	US-09-908-975-21728	Sequence 21728, A
C 431	11.8	56.2	50	13	US-09-903-562-79	Sequence 79, Appl	C 504	11.6	55.2	64	11	US-09-950-920-8	Sequence 8, Appl
C 432	11.8	56.2	50	13	US-09-904-877A-79	Sequence 79, Appl	C 505	11.6	55.2	64	11	US-10-027-632-58365	Sequence 58365, A
C 433	11.8	56.2	50	13	US-10-299-937-79	Sequence 79, Appl	C 506	11.6	55.2	64	14	US-10-027-632-58365	Sequence 58365, A
C 434	11.8	56.2	50	13	US-09-906-618-79	Sequence 79, Appl	C 507	11.6	55.2	65	13	US-09-908-975-1594	Sequence 1594, Ap
C 435	11.8	56.2	50	13	US-09-907-128-79	Sequence 79, Appl	C 508	11.6	55.2	65	13	US-09-908-975-3090	Sequence 3090, Ap
C 436	11.8	56.2	50	13	US-09-904-805-79	Sequence 79, Appl	C 509	11.6	55.2	65	13	US-09-908-975-26477	Sequence 26477, A
C 437	11.8	56.2	50	13	US-09-904-938A-79	Sequence 79, Appl	C 510	11.6	55.2	65	13	US-09-908-975-28020	Sequence 28020, A
C 438	11.8	56.2	50	13	US-09-906-722A-79	Sequence 79, Appl	C 511	11.6	55.2	65	13	US-10-032-585-315	Sequence 315, App
C 439	11.8	56.2	55	9	US-09-860-996-23	Sequence 23, Appl	C 512	11.6	55.2	65	13	US-10-032-585-2565	Sequence 2565, Ap
C 440	11.8	56.2	60	10	US-09-832-659-9	Sequence 9, Appl	C 513	11.6	55.2	65	13	US-10-032-585-2793	Sequence 2793, Ap
C 441	11.8	56.2	60	11	US-09-832-658-3	Sequence 3, Appl	C 514	11.6	55.2	65	13	US-10-032-585-3018	Sequence 3018, Ap
C 442	11.8	56.2	60	11	US-09-908-975-5855	Sequence 5855, Ap	C 515	11.6	55.2	66	10	US-09-854-999-45	Sequence 45, Appl
C 443	11.8	56.2	60	13	US-09-908-975-15921	Sequence 15921, A	C 516	11.6	55.2	68	11	US-09-866-925-246	Sequence 246, App
C 444	11.8	56.2	60	13	US-09-908-975-18456	Sequence 18456, A	C 517	11.6	55.2	69	11	US-09-951-061A-4	Sequence 4, Appl
C 445	11.8	56.2	64	9	US-09-923-876-3468	Sequence 3468, Ap	C 518	11.6	55.2	72	13	US-10-267-884-4	Sequence 72, Appl
C 446	11.8	56.2	64	12	US-09-923-876-3468	Sequence 3468, Ap	C 519	11.6	55.2	72	13	US-10-159-006-72	Sequence 72, Appl
C 447	11.8	56.2	65	13	US-09-908-975-24580	Sequence 24580, A	C 520	11.6	55.2	72	13	US-10-027-632-176001	Sequence 176001, A
C 448	11.8	56.2	65	13	US-09-908-975-24580	Sequence 24580, A	C 521	11.6	55.2	74	14	US-10-027-632-176001	Sequence 176001, A
C 449	11.8	56.2	65	14	US-09-908-975-29552	Sequence 29552, A	C 522	11.6	55.2	74	14	US-10-027-632-176001	Sequence 28074, A
C 450	11.8	56.2	65	14	US-10-021-758-17	Sequence 17, Appl	C 523	11.6	55.2	75	9	US-09-864-761-28074	Sequence 28074, A
C 451	11.8	56.2	83	10	US-09-783-590-9721	Sequence 9721, Ap	C 524	11.6	55.2	78	8	US-08-781-986A-4894	Sequence 4894, Ap
C 452	11.8	56.2	90	10	US-09-867-701-1274	Sequence 1274, Ap	C 525	11.6	55.2	79	9	US-09-864-761-19195	Sequence 19195, A
C 453	11.6	55.2	20	9	US-09-802-669-174	Sequence 174, App	C 526	11.6	55.2	79	9	US-09-864-761-19195	Sequence 19195, A

527	11.6	55.2	79	9	US-09-864-761-19717	Sequence 19717, A	600	11.4	54.3	50	10	US-09-999-832A-521	Sequence 521, App
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C 529	11.6	55.2	82	9	US-09-864-761-26051	Sequence 26051, A	C 602	11.4	54.3	50	11	US-09-924-366A-7	Sequence 7, Appl1
C 530	11.6	55.2	87	11	US-09-213-932A-4	Sequence 4, Appl1	C 603	11.4	54.3	50	11	US-09-924-366A-10	Sequence 10, Appl1
C 531	11.6	55.2	100	12	US-10-242-535A-54256	Sequence 54256, A	604	11.4	54.3	50	11	US-09-978-608A-521	Sequence 521, App
C 532	11.6	55.2	100	12	US-10-242-535A-54450	Sequence 54450, A	605	11.4	54.3	50	11	US-09-978-585A-521	Sequence 521, App
C 533	11.4	54.3	15	13	US-10-440-850-849	Sequence 849, App	606	11.4	54.3	50	11	US-09-978-191A-521	Sequence 521, App
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535	11.4	54.3	20	10	US-09-924-417-6	Sequence 6, Appl1	608	11.4	54.3	50	11	US-09-978-564A-521	Sequence 521, App
C 536	11.4	54.3	20	11	US-09-824-322B-352	Sequence 352, App	609	11.4	54.3	50	11	US-09-999-833A-521	Sequence 521, App
C 537	11.4	54.3	20	11	US-09-824-322B-356	Sequence 356, App	610	11.4	54.3	50	11	US-09-981-915A-521	Sequence 521, App
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539	11.4	54.3	20	13	US-10-186-950-42	Sequence 42, Appl1	612	11.4	54.3	50	11	US-09-918-885A-521	Sequence 521, App
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545	11.4	54.3	22	9	US-09-874-626-6	Sequence 6, Appl1	618	11.4	54.3	50	11	US-09-978-643A-521	Sequence 521, App
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C 551	11.4	54.3	25	12	US-09-927-876-64	Sequence 64, Appl1	C 624	11.4	54.3	50	12	US-10-131-827-2049	Sequence 2049, App
C 552	11.4	54.3	25	13	US-10-360-149-64	Sequence 64, Appl1	C 625	11.4	54.3	50	12	US-10-131-827-2248	Sequence 2248, App
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C 560	11.4	54.3	25	15	US-10-098-263B-40312	Sequence 40312, App	633	11.4	54.3	50	13	US-09-978-188A-521	Sequence 521, App
561	11.4	54.3	25	15	US-10-098-263B-41806	Sequence 41806, App	634	11.4	54.3	50	13	US-09-978-298A-521	Sequence 521, App
562	11.4	54.3	25	15	US-10-098-263B-42395	Sequence 42395, App	635	11.4	54.3	50	13	US-10-143-031A-521	Sequence 521, App
C 563	11.4	54.3	25	15	US-10-098-263B-50648	Sequence 50648, App	636	11.4	54.3	50	13	US-10-002-967A-521	Sequence 521, App
564	11.4	54.3	25	15	US-10-098-263B-84449	Sequence 84449, App	637	11.4	54.3	50	13	US-10-017-083A-521	Sequence 521, App
565	11.4	54.3	25	15	US-10-098-263B-88081	Sequence 88081, App	638	11.4	54.3	50	13	US-10-143-030A-521	Sequence 521, App
C 566	11.4	54.3	25	15	US-10-098-263B-89306	Sequence 89306, App	639	11.4	54.3	50	13	US-10-145-128A-521	Sequence 521, App
C 567	11.4	54.3	25	15	US-10-098-263B-100715	Sequence 100715, App	640	11.4	54.3	50	13	US-10-017-191A-521	Sequence 521, App
568	11.4	54.3	25	15	US-10-098-263B-101696	Sequence 101696, App	641	11.4	54.3	50	13	US-10-143-028A-521	Sequence 521, App
569	11.4	54.3	25	15	US-10-098-263B-114893	Sequence 114893, App	642	11.4	54.3	50	13	US-10-143-029A-521	Sequence 521, App
570	11.4	54.3	25	15	US-10-098-263B-117712	Sequence 117712, App	643	11.4	54.3	50	13	US-10-145-089A-521	Sequence 521, App
C 571	11.4	54.3	25	15	US-10-098-263B-117737	Sequence 117737, App	644	11.4	54.3	50	13	US-10-013-926A-521	Sequence 521, App
C 572	11.4	54.3	25	15	US-10-098-263B-119106	Sequence 119106, App	645	11.4	54.3	50	13	US-10-145-078A-521	Sequence 521, App
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C 574	11.4	54.3	26	9	US-09-402-100-46	Sequence 46, Appl1	647	11.4	54.3	50	13	US-10-145-124A-521	Sequence 521, App
C 575	11.4	54.3	29	15	US-10-153-363A-41	Sequence 41, Appl1	648	11.4	54.3	50	13	US-10-160-502A-521	Sequence 521, App
576	11.4	54.3	29	15	US-10-153-363A-42	Sequence 42, Appl1	649	11.4	54.3	50	13	US-10-165-247A-521	Sequence 521, App
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C 578	11.4	54.3	30	14	US-10-147-342-7	Sequence 7, Appl1	651	11.4	54.3	50	13	US-09-978-194A-521	Sequence 521, App
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C 587	11.4	54.3	42	15	US-10-015-535-14	Sequence 14, Appl1	660	11.4	54.3	50	13	US-09-978-544A-521	Sequence 521, App
588	11.4	54.3	43	13	US-10-032-585-885	Sequence 885, App	661	11.4	54.3	50	13	US-09-978-665A-521	Sequence 521, App
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593	11.4	54.3	47	10	US-09-944-243-7	Sequence 7, Appl1	666	11.4	54.3	50	13	US-10-013-919A-521	Sequence 521, App
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599	11.4	54.3	50	10	US-09-978-192A-521	Sequence 521, App	672	11.4	54.3	50	13	US-10-013-927A-521	Sequence 521, App

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675	11.4	54.3	50	15	US-10-017-081A-521	Sequence 521, App	C 748	11.4	54.3	86	9	US-09-915-593-19	Sequence 19, Appli
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C 683	11.4	54.3	60	13	US-09-908-975-5315	Sequence 5315, Ap	C 756	11.4	54.3	86	10	US-09-764-873-3	Sequence 3, Appli
C 684	11.4	54.3	60	13	US-09-908-975-7493	Sequence 7493, Ap	C 757	11.4	54.3	86	10	US-09-925-300-1883	Sequence 1883, Ap
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C 988 11.2 53.3 40 14 US-10-027-632-175486 Sequence 175486,
C 989 11.2 53.3 41 9 US-09-782-361-18 Sequence 18, Appl
C 990 11.2 53.3 42 13 US-09-996-008B-5 Sequence 5, Appl
C 991 11.2 53.3 43 13 US-10-032-585-1694 Sequence 1694, Ap
C 992 11.2 53.3 44 9 US-09-782-361-19 Sequence 19, Appl
C 993 11.2 53.3 45 11 US-09-491-322-4 Sequence 4, Appl
C 994 11.2 53.3 45 13 US-10-372-614-4 Sequence 4, Appl
C 995 11.2 53.3 45 13 US-10-374-603-4 Sequence 4, Appl
C 996 11.2 53.3 47 12 US-10-349-143-2964 Sequence 2964, Ap
C 997 11.2 53.3 47 12 US-10-349-143-3290 Sequence 3290, Ap
C 998 11.2 53.3 47 12 US-10-455-013-9 Sequence 8, Appl
C 999 11.2 53.3 47 12 US-10-455-013-9 Sequence 9, Appl
C1000 11.2 53.3 47 12 US-10-455-013-12 Sequence 12, Appl
```

## ALIGNMENTS

```
RESULT 1
US-09-954-987B-30
; Sequence 30, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Wagner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AWS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-954-987B-30
```

Query Match 85.7%; Score 18; DB 11; Length 20;

```
Best Local Similarity 100.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGATTCTAGGAATTCAA 18
Db 1 AGATTCTAGGAATTCAA 18
```

## RESULT 2

```
US-09-877-705A-91
; Sequence 91, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP91
US-09-877-705A-91
```

Query Match 85.7%; Score 18; DB 11; Length 21;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AGATTCTAGGAATTCAA 18
Db 1 AGATTCTAGGAATTCAA 18
```

## RESULT 3

```
US-09-877-705A-92/C
; Sequence 92, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIPT
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP92
US-09-877-705A-92
```

Query Match 85.7%; Score 18; DB 11; Length 21;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AGATTCTAGGAATTCAA 18
Db 21 AGATTCTAGGAATTCAA 4
```

## RESULT 4

```
US-09-877-738A-91
; Sequence 91, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP91
US-09-877-738A-91

Query Match
; Sequence 92, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP92
US-09-877-738A-92

Query Match
; Sequence 18, DB 11, Length 21,
; Best Local Similarity 100.0%; Pred. No. 70;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 1 AGATTCTAGGAATTCAA 18

RESULT 5
US-09-877-738A-92/C
; Sequence 92, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Transcription factor probe PP92
US-09-877-738A-92

Query Match
; Sequence 18, DB 11, Length 21,
; Best Local Similarity 100.0%; Pred. No. 70;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 21 AGATTCTAGGAATTCAA 4

RESULT 6
US-09-877-705A-154/C
; Sequence 154, Application US/09877705A
; Publication No. US20030008283A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD FOR SCREENING FOR DRUG CANDIDATES FOR MODULATING TRANSCRIP
; FILE OF INVENTION: FACTOR ACTIVITY
; FILE REFERENCE: 26757-704
; CURRENT APPLICATION NUMBER: US/09/877,705A
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Hybridization probe MP92
US-09-877-705A-154

Query Match
; Sequence 18, DB 11, Length 63;
; Best Local Similarity 100.0%; Pred. No. 87;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 63 AGATTCTAGGAATTCAA 46

RESULT 7
US-09-877-738A-154/C
; Sequence 154, Application US/09877738A
; Publication No. US20030022173A1
; GENERAL INFORMATION:
; APPLICANT: Li, Jason
; TITLE OF INVENTION: METHOD AND KIT FOR ISOLATING DNA PROBES THAT BIND TO ACTIVATED
; FILE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: 26757-701
; CURRENT APPLICATION NUMBER: US/09/877,738A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Hybridization probe MP92
US-09-877-738A-154

Query Match
; Sequence 18, DB 11, Length 63;
; Best Local Similarity 100.0%; Pred. No. 87;
; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18
DB 63 AGATTCTAGGAATTCAA 46

RESULT 8
US-09-923-246-59
; Sequence 59, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1k, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial sequence
```

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12749
US-09-923-246-59
Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      67 AGATTCTAGGAATTCAA 84

RESULT 9
US-09-923-246-60/c
; Sequence 60, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey K.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12748
US-09-923-246-60

Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      38 AGATTCTAGGAATTCAA 21

RESULT 10
US-09-825-561A-48
; Sequence 48, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
```

```
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12749
US-09-825-561A-48

Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      67 AGATTCTAGGAATTCAA 84

RESULT 11
US-09-825-561A-49/c
; Sequence 49, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12748
US-09-825-561A-49

Query Match      85.7%; Score 18; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
Db      38 AGATTCTAGGAATTCAA 21

RESULT 12
US-09-892-949-43
; Sequence 43, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
```



```

; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12749
US-09-892-949-43
```

```

Query Match      85.7%; Score 18; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AGATTCTAGGAATTCAA 18
        |||
Db      67 AGATTCTAGGAATTCAA 84
```

```

RESULT 13
US-09-892-949-44/c
; Sequence 44, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark E.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12748
US-09-892-949-44
```

```

Query Match      85.7%; Score 18; DB 11; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AGATTCTAGGAATTCAA 18
        |||
Db      38 AGATTCTAGGAATTCAA 21
```

```

RESULT 14
US-10-282-622-17
; Sequence 17, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
```

```

; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC12,749
US-10-282-622-17
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```

Query Match      85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AGATTCTAGGAATTCAA 18
        |||
Db      67 AGATTCTAGGAATTCAA 84
```

```

RESULT 15
US-10-282-622-18/c
; Sequence 18, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC12,748
US-10-282-622-18
```

```

Query Match      85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AGATTCTAGGAATTCAA 18
        |||
Db      38 AGATTCTAGGAATTCAA 21
```

```

RESULT 16
US-10-351-157-44
; Sequence 44, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
```

```

; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12749
; US-10-351-157-44

Query Match      85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
        |||
        67 AGATTCTAGGAATTCAA 84

RESULT 17
; US-10-351-157-45/c
; Sequence 45, Application US/10351157
; Publication No. US20030215838A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Gao, Zeren
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Dasovich, Maria M.
; APPLICANT: Grant, Francis J.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Hammond, Angela K.
; APPLICANT: No. US20030215838A1ak, Julia E.
; APPLICANT: Gross, Jane A.
; APPLICANT: Dillon, Stacey R.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17 MULTIMERS
; FILE REFERENCE: 02-02
; CURRENT APPLICATION NUMBER: US/10/351,157
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/435,361
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/389,108
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/350,325
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC12748
; US-10-351-157-45

Query Match      85.7%; Score 18; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
        |||
        67 AGATTCTAGGAATTCAA 84
```

```

; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC12749
; US-10-295-723-59

Query Match      85.7%; Score 18; DB 15; Length 100;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGATTCTAGGAATTCAA 18
        |||
        67 AGATTCTAGGAATTCAA 84

RESULT 19
; US-10-295-723-60/c
; Sequence 60, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
```

PRIOR APPLICATION NUMBER: US 60/123,904  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: US 60/142,013  
PRIOR FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 100  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide ZC12748  
US-10-295-723-60

Query Match 85.7%; Score 18; DB 15; Length 100;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTCAA 18  
Db 38 AGATTCTAGGAATTCAA 21

RESULT 20  
US-10-325-606-1/c  
Sequence 1, Application US/10325606  
Publication No. US20030216295A1  
GENERAL INFORMATION:

APPLICANT: FUKUDA, MINORU  
SAMADA, RITSUKO  
TSUBOI, SHIGERU

TITLE OF INVENTION: E-SELECTIN-DEPENDENT CELL ADHESION  
ANTAGONISTS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE. 700  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/325,606  
FILING DATE: 20-Dec-2002  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/369,754  
FILING DATE: 06-JAN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN  
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 1113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-9001  
TELEFAX: 619-535-8949

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-325-606-1

Query Match 73.3%; Score 15.4; DB 13; Length 24;  
Best Local Similarity 94.1%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAA 19  
Db 17 ATTCTAGGAATTCAA 1

RESULT 21

US-10-327-481A-21/c  
Sequence 21, Application US/10327481A  
Publication No. US20040001864A1  
GENERAL INFORMATION:

APPLICANT: King, Andrew M.O.  
APPLICANT: Burman, Allison J.  
APPLICANT: Audonnet, Jean-Christophe F.

TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease  
FILE REFERENCE: 454313-3178

CURRENT APPLICATION NUMBER: US/10/327,481A  
CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: PCT/FR01/02042  
PRIOR FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: FR 0008437  
PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 21

LENGTH: 41  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:

OTHER INFORMATION: a fragment of about 3470 bp  
US-10-327-481A-21

Query Match 70.5%; Score 14.8; DB 12; Length 41;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATTCAA 19  
Db 19 GATTCTAGGAATTCAA 2

RESULT 22

US-10-327-481A-23/c  
Sequence 23, Application US/10327481A  
Publication No. US20040001864A1  
GENERAL INFORMATION:

APPLICANT: King, Andrew M.O.  
APPLICANT: Burman, Allison J.

APPLICANT: Audonnet, Jean-Christophe F.  
APPLICANT: Lombard, Michel F.A.

TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease  
FILE REFERENCE: 454313-3178

CURRENT APPLICATION NUMBER: US/10/327,481A  
CURRENT FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: PCT/FR01/02042  
PRIOR FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: FR 0008437  
PRIOR FILING DATE: 2000-06-29

NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 23

LENGTH: 41  
TYPE: DNA

ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: a fragment of about 3460 bp

US-10-327-481A-23

Query Match 70.5%; Score 14.8; DB 12; Length 41;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATTTCTAGGAATTCAAA 19  
Db 19 GATTTTATGAAATTCAAA 2

## RESULT 23

US-10-327-481A-19/C  
; Sequence 19, Application US/10327481A  
; Publication No. US20040001864A1  
; GENERAL INFORMATION:  
; APPLICANT: King, Andrew M.O.  
; APPLICANT: Burman, Alison J.  
; APPLICANT: Audonnet, Jean-Christophe F.  
; APPLICANT: Lombard, Michel F.A.  
; TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease  
; FILE REFERENCE: 454313-3178  
; CURRENT APPLICATION NUMBER: US/10/327,481A  
; PRIOR FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: PCT/FR01/02042  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: FR 0008437  
; PRIOR FILING DATE: 2000-06-29  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: a oligonucleotide JCA323 used in PCR in example 6 to amplify  
US-10-327-481A-19  
Query Match 70.5%; Score 14.8; DB 12; Length 44;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GATTTCTAGGAATTCAAA 19  
Db 19 GATTTTATGAAATTCAAA 2

## RESULT 24

US-10-327-481A-25/C  
; Sequence 25, Application US/10327481A  
; Publication No. US20040001864A1  
; GENERAL INFORMATION:  
; APPLICANT: King, Andrew M.O.  
; APPLICANT: Burman, Alison J.  
; APPLICANT: Audonnet, Jean-Christophe F.  
; APPLICANT: Lombard, Michel F.A.  
; TITLE OF INVENTION: Vaccine against Foot-and-Mouth Disease  
; FILE REFERENCE: 454313-3178  
; CURRENT APPLICATION NUMBER: US/10/327,481A  
; PRIOR FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: PCT/FR01/02042  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: FR 0008437  
; PRIOR FILING DATE: 2000-06-29  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: a oligonucleotide JCA329 used in PCR in example 7 to amplify  
US-10-327-481A-25  
Query Match 70.5%; Score 14.8; DB 12; Length 44;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GATTTCTAGGAATTCAAA 19  
Db 19 GATTTTATGAAATTCAAA 2

## RESULT 25

US-09-932-679-42  
; Sequence 42, Application US/09932679  
; Patent No. US20020058801A1  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: No. US20020058801A1ak, Julia R.  
; TITLE OF INVENTION: Mammalian Alpha Helical Protein-1  
; FILE REFERENCE: 97-71D1  
; CURRENT APPLICATION NUMBER: US/09/932,679  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: 09/209,525  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/067,779  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 58  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-932-679-42

Query Match 69.5%; Score 14.6; DB 9; Length 58;  
Best Local Similarity 81.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 AGATTTCTAGGAATTCAAATC 21  
Db 14 AGAATCTAGGAATTCCTACTC 34

## RESULT 26

US-10-197-293-46  
; Sequence 46, Application US/10197293  
; Publication No. US20030171547A1  
; GENERAL INFORMATION:  
; APPLICANT: Shepard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49C1  
; CURRENT APPLICATION NUMBER: US/10/197,293  
; PRIOR FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: US 09/686,838  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/140,804  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/056,983  
; PRIOR FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 58  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC14819  
US-10-197-293-46

Query Match 69.5%; Score 14.6; DB 13; Length 58;  
Best Local Similarity 81.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 AGATTTCTAGGAATTCAAATC 21

Db 14 AGAATCTAGGAATCTATTC 34

## RESULT 27

US-09-969-373-1158/c  
; Sequence 1158, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Efferetz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SRS and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 1158  
; LENGTH: 99  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-1158

## Query Match

Best Local Similarity 67.6%; Score 14.2; DB 10; Length 99;  
Best Local Similarity 84.2%; Pred. No. 5.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATTCTAGGAATTCATTC 21  
Db 60 ATTATATGAAITGAAATC 42

## RESULT 28

US-09-908-975-14277/c  
; Sequence 14277, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Itat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; PRIOR FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14277  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-14277

## Query Match

Best Local Similarity 66.7%; Score 14; DB 13; Length 60;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATTTCTAGGAATT 15  
Db 52 GATTTCTAGGAATT 39

## RESULT 29

US-09-920-033-115/c

; Sequence 115, Application US/09920033  
; Publication No. US20030087853A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosanne M. Crooke  
; APPLICANT: Mark J. Graham  
; TITLE OF INVENTION: ANTISENSE MODULATION OF ABOLIPROTEIN B EXPRESSION  
; FILE REFERENCE: ISPH-0592  
; CURRENT APPLICATION NUMBER: US/09/920,033  
; PRIOR FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 123  
; SEQ ID NO 115  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-920-033-115

## Query Match

Best Local Similarity 65.7%; Score 13.8; DB 11; Length 20;  
Best Local Similarity 88.2%; Pred. No. 6.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GATTTCTAGGAATTC 18  
Db 20 GATTTCAAGGATTC 4

## RESULT 30

US-10-388-263-651/c  
; Sequence 651, Application US/10388263  
; Publication No. US20030228597A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowseert, Lex M.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: McNeil, John  
; APPLICANT: Freier, Susan M.  
; APPLICANT: Sasnor, Henri M.  
; APPLICANT: Brooks, Douglas G.  
; APPLICANT: Ohashi, Cara  
; APPLICANT: Wyatt, Jacqueline R.  
; APPLICANT: Borchers, Alexander  
; APPLICANT: Vickers, Timothy A.  
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR  
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND  
; FILE REFERENCE: 151S-4503  
; CURRENT APPLICATION NUMBER: US/10/388,263  
; PRIOR FILING DATE: 2003-03-12  
; NUMBER OF SEQ ID NOS: 947  
; SOFTWARE: FASTSBQ for Windows Version 4.0  
; SEQ ID NO 651  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-388-263-651

## Query Match

Best Local Similarity 65.7%; Score 13.8; DB 12; Length 20;  
Best Local Similarity 88.2%; Pred. No. 6.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GATTTCTAGGAATTC 18  
Db 20 GATTTCAAGGATTC 4

## RESULT 31

US-10-147-196-115/c  
; Sequence 115, Application US/10147196  
; Publication No. US20030215943A1  
; GENERAL INFORMATION:

```

; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark U. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLOPROTEIN B EXPRESSION
; FILE REFERENCE: ISPH-0664
; CURRENT APPLICATION NUMBER: US/10/147,196
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 124
; SEQ ID NO 115
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-147-196-115

Query Match      65.7%; Score 13.8; DB 13; Length 20;
Best Local Similarity 88.2%; Pred. No. 6.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GATTTCTAGGAATTCGA 18
Db      20 GATTTCAAGGGAATTCGA 4

RESULT 32
US-09-908-975-20387
; Sequence 20387, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSEMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20387
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-20387

Query Match      65.7%; Score 13.8; DB 13; Length 60;
Best Local Similarity 88.2%; Pred. No. 8.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGATTTCTAGGAATTCGA 17
Db      33 AGCTTCTGGGAATTCGA 49

RESULT 33
US-09-908-975-30132/c
; Sequence 30132, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: MASSEMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
```

```

; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30132
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-908-975-30132

Query Match      65.7%; Score 13.8; DB 13; Length 65;
Best Local Similarity 88.2%; Pred. No. 8.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 TTCTAGGAATTCGAATC 21
Db      62 TTCTAGGAATTCGAGTC 46

RESULT 34
US-10-098-263B-26232/c
; Sequence 26232, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Maltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 26232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-26232

Query Match      64.8%; Score 13.6; DB 15; Length 25;
Best Local Similarity 80.0%; Pred. No. 8.6e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 AGATTTCTAGGAATTCGAAT 20
Db      20 AGATATATAGTAATTCACAT 1

RESULT 35
US-10-307-441-42
; Sequence 42, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; TITLE OF INVENTION: Modified Research Council of Canada
; FILE REFERENCE: 027367-50060S
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 44
; TYPE: DNA
```

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Tx-C1  
US-10-307-441-42

Query Match 64.8%; Score 13.6; DB 13; Length 44;  
Best Local Similarity 80.0%; Pred. No. 9.5e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GATTCTAGGAATTCGAATC 21  
Db 24 GATTCTAGGAATTCGAATC 43

RESULT 36  
US-09-927-876-69/c

Sequence 69, Application US/09927876  
Publication No. US2004000554A1  
GENERAL INFORMATION:  
APPLICANT: El Tayar, Nabli  
APPLICANT: Campbell, Robert K  
APPLICANT: Kelton, Christie A  
APPLICANT: He, Chaomei  
TITLE OF INVENTION: No. US2004000554A1el Glycoproteins and Methods of Use Thereof  
FILE REFERENCE: 20993-003  
CURRENT APPLICATION NUMBER: US/09/927,876  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/225,035  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/202,724  
PRIOR FILING DATE: 2000-05-08  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 69  
LENGTH: 28  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
US-09-927-876-69

Query Match 63.8%; Score 13.4; DB 12; Length 28;  
Best Local Similarity 93.3%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTCTAGGAATTCGAA 19  
Db 16 TACTAGGAATTCGAA 2

RESULT 37

US-10-360-149-69/c  
Sequence 69, Application US/10360149  
Publication No. US20030219786A1  
GENERAL INFORMATION:  
APPLICANT: El Tayar, Nabli  
APPLICANT: Campbell, Robert K  
APPLICANT: Kelton, Christie A  
APPLICANT: He, Chaomei  
TITLE OF INVENTION: No. US20030219786A1el Glycoproteins and Methods of Use Thereof  
FILE REFERENCE: 20993-003  
CURRENT APPLICATION NUMBER: US/10/360,149  
CURRENT FILING DATE: 2003-02-06  
PRIOR APPLICATION NUMBER: US/09/927,876  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/225,035  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/202,724  
PRIOR FILING DATE: 2000-05-08  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 69

LENGTH: 28  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
US-10-360-149-69

Query Match 63.8%; Score 13.4; DB 13; Length 28;  
Best Local Similarity 93.3%; Pred. No. 1.1e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TTCTAGGAATTCGAA 19  
Db 16 TACTAGGAATTCGAA 2

RESULT 38

US-09-908-975-28326/c  
Sequence 28326, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Lat  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 28326  
LENGTH: 65  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-908-975-28326

Query Match 63.8%; Score 13.4; DB 13; Length 65;  
Best Local Similarity 93.3%; Pred. No. 1.3e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GATTCTAGGAATTC 16  
Db 58 GATTCTAGGAATTC 44

RESULT 39

US-10-251-117-633/c  
Sequence 633, Application US/10251117  
Publication No. US20030170891A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: MCSwiggan, James  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R  
FILE REFERENCE: 900/042 (MBHB02-468-A)  
CURRENT APPLICATION NUMBER: US/10/251,117  
CURRENT FILING DATE: 2003-02-24  
PRIOR APPLICATION NUMBER: US 60/393,924  
PRIOR FILING DATE: 2002-07-03  
PRIOR APPLICATION NUMBER: US 10/163,552  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 09/916,466  
PRIOR FILING DATE: 2001-07-25

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/ PRIOR APPLICATION NUMBER: US 60/296,249
/ PRIOR FILING DATE: 2001-06-06
/ NUMBER OF SEQ ID NOS: 1213
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 633
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-251-117-633

Query Match      62.9%; Score 13.2; DB 13; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GATTCTAGAGAAATTCAAA 19
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Db      19 GATTCTAGTCTCATA 2

RESULT 40
US-10-251-117-940
/ Sequence 940, Application US/10251117
/ Publication No. US20030170891A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: MCSwigen, James
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
/ TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
/ FILE REFERENCE: 900/042 (MBH802-468-A)
/ CURRENT APPLICATION NUMBER: US/10/251,117
/ PRIOR FILING DATE: 2003-02-24
/ PRIOR APPLICATION NUMBER: US 60/393,924
/ PRIOR FILING DATE: 2002-07-03
/ PRIOR APPLICATION NUMBER: US 10/163,552
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 09/916,466
/ PRIOR FILING DATE: 2001-07-25
/ PRIOR APPLICATION NUMBER: US 60/296,249
/ PRIOR FILING DATE: 2001-06-06
/ NUMBER OF SEQ ID NOS: 1213
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 940
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-940

Query Match      62.9%; Score 13.2; DB 13; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.3e+04;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 GATTCTAGAGAAATTCAAA 19
        |||||
Db      1 GAUUUCUAGGUUCUCAA 18

Search completed: February 4, 2004, 19:45:55
Job time : 151.409 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 15:19:23 / Search time 1185.23 Seconds  
(without alignments)  
430.630 Million cell updates/sec

Title: US-09-744-875A-1

Sequence: 1 agattctcgaatcaatc 21

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 452990

Minimum DB seq length: 0  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : EST.\*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estor:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_plh:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	15.2	72.4	87	14	CB405258 OSTR040A2

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C	6	15.2	72.4	93	13	B0837156	B0837156 T095D05 P
C	7	15.2	72.4	97	13	B0890262	B0890262 P034B05 P
C	8	14.6	69.5	73	9	AA749115	AA749115 oas8g04.s
C	9	14.6	69.5	93	29	BZ593365	BZ593365 SALK_0703
C	10	14.4	68.6	63	9	AM695026	AM695026 NF082E06S
C	11	14.4	68.6	93	14	CA513671	CA513671 10-3_1h2
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C	13	14.2	67.6	48	28	BH851999	BH851999 SALK_0740
C	14	14.2	67.6	60	10	BG153679	BG153679 nag58g908
C	15	14.2	67.6	83	9	AI966296	AI966296 sc36h04.y
C	16	13.8	65.7	47	12	B0707154	B0707154 B0707154
C	17	13.8	65.7	49	9	AA422541	AA422541 v14c03.s
C	18	13.8	65.7	69	28	A2810918	A2810918 2M0076K14
C	19	13.8	65.7	69	28	A2956832	A2956832 2M0223C05
C	20	13.8	65.7	76	10	BG153467	BG153467 nag49a01.
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C	22	13.8	65.7	88	10	BG151856	BG151856 nag65d05.
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C	27	13.6	64.8	48	10	BH789276	BH789276 B000015-3
C	28	13.6	64.8	50	10	BF463652	BF463652 UI-M-CG0P
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C	30	13.6	64.8	71	10	B0890627	B0890627 P039E04 P
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C	35	13.6	64.8	91	13	B0890255	D75616
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C	37	13.6	64.8	94	28	BM181183	BM181183 1006077E0
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C	39	13.6	64.8	96	29	CNS00DHH	BZ32958 SALK_1195
C	40	13.6	64.8	100	29	BZ32958	BZ382706 SALK_1187
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C	47	13.2	62.9	61	28	BH218412	AU011284 AU011284
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C	54	13.2	62.9	89	9	AW712808	BH218396 1006078F0
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C	66	13.2	62.9	41	29	BZ538843	BH791798 SALK_0613
C	67	13	61.9	47	28	BH791798	AI452866 T. bncei
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C	69	13	61.9	68	29	DR21G925	BZ593307 SALK_0699
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C	71	13	61.9	74	28	B0813172	AL945129 Arabidops
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C	74	13	61.9	81	29	BZ593444	BZ592972 SALK_0514
C	75	13	61.9	83	28	BH609015	BZ706390
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78	13	61.9	85	29	BZ593630	SALK_0749
79	13	61.9	86	29	BZ770275	SALK_1432
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81	13	61.9	88	28	BH790508	SALK_0572
82	13	61.9	89	29	BZ593430	SALK_0704
83	13	61.9	90	29	BZ593430	SALK_0738
84	13	61.9	91	28	BH813401	SALK_0641
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86	13	61.9	91	29	BZ593608	SALK_0749
87	13	61.9	91	29	BZ593615	SALK_0749
88	13	61.9	93	14	CA802671	SAU40C07.
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90	13	61.9	93	29	BZ593225	SALK_0682
91	13	61.9	93	29	BZ593350	SALK_0700
92	13	61.9	94	10	BE317003	NF058031
93	13	61.9	94	10	BE317003	NF058031
94	13	61.9	94	29	BZ596785	SALK_0959
95	13	61.9	94	29	BZ597388	SALK_1035
96	13	61.9	94	29	BZ597388	SALK_1035
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102	13	61.9	97	29	BZ593339	SALK_0700
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105	13	61.9	98	29	BZ596790	SALK_0960
106	13	61.9	99	29	BZ592969	SALK_0514
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108	13	61.9	100	9	AA123114	mm30g03.r
109	13	61.9	100	29	BZ593475	SALK_0738
110	13	61.9	100	29	BZ593514	SALK_0739
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113	12.8	61.0	59	14	D19098	MUSG801305
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116	12.8	61.0	79	12	BI749369	ro77c09.Y
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231	12.2	58.1	90	29	BX227157	BX227157 Danilo rer	304	12	57.1	73	14	CD400293	CD400293 gm ck2213
232	12.2	58.1	91	9	AA886069	AA886069 ny40e08.s	305	12	57.1	74	9	AA961856	AA961856 org f01.s
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247	12.2	58.1	96	9	AF211554	AF211554 AF211554	320	12	57.1	81	29	AL951913	AL951913 Arabidops
248	12.2	58.1	96	9	AV970576	AV970576 AV970576	321	12	57.1	81	29	AM546050	AM546050 l0001F05-
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C 519	11.6	55.2	81	12	BM436075	BM436075 IRu20E1.a	C 592	11.6	55.2	99	28	BH910534	BH910534 SALK 0601
C 520	11.6	55.2	81	14	CA856618	CA856618 PESTOAC1	C 593	11.6	55.2	99	29	CC455417	CC455417 SALK 0821
C 521	11.6	55.2	82	9	AJ499243	AJ499243	C 594	11.6	55.2	99	29	CC456126	CC456126 SALK 0936
C 522	11.6	55.2	82	28	BH909257	BH909257 SALK 0526	C 595	11.6	55.2	99	29	AG242456	AG242456 Lotus Jap
C 523	11.6	55.2	82	29	CC056562	CC056562 SALK 1087	C 596	11.6	55.2	100	10	BG142713	BG142713 ve61c07.r
C 524	11.6	55.2	82	29	CC456294	CC456294 SALK 0970	C 597	11.6	55.2	100	10	BG657485	BG657485 T08T2742
C 525	11.6	55.2	83	9	AA606588	AA606588 vm8b03.r	C 598	11.6	55.2	100	14	CA844430	CA844430 BSSSRG 1B
C 526	11.6	55.2	83	29	CC179387	CC179387 SALK 0681	C 599	11.6	55.2	100	10	BE074143	BE074143 RC4-BT056
C 527	11.6	55.2	83	29	AL942410	AL942410 Arabidops	C 600	11.6	55.2	100	14	CA844430	CA844430 BSSSRG 1C
C 528	11.6	55.2	84	12	BM276486	BM276486 PESTOAC6	C 601	11.6	55.2	100	14	CA844430	CA844430 BSSSRG 1C
C 529	11.6	55.2	84	13	B0866619	B0866619 S068H03 P	C 602	11.4	54.3	23	29	BZ357850	BZ357850 SALK 1313
C 530	11.6	55.2	84	14	CA854531	CA854531 PESTOAC3	C 603	11.4	54.3	26	28	AZ779345	AZ779345 SALK 1026
C 531	11.6	55.2	84	14	CA854531	CA854531 PESTOAC3	C 604	11.4	54.3	32	28	AZ793545	AZ793545 2M0012C23
C 532	11.6	55.2	84	14	CA854531	CA854531 PESTOAC3	C 605	11.4	54.3	33	28	AZ340354	AZ340354 1M0072P06
C 533	11.6	55.2	84	28	BH910242	BH910242 SALK 0585	C 606	11.4	54.3	34	28	BH813789	BH813789 SALK 0653
C 534	11.6	55.2	84	28	BZ660586	BZ660586 SALK 0240	C 607	11.4	54.3	35	28	AZ345589	AZ345589 1M0080N16
C 535	11.6	55.2	85	14	CD415624	CD415624 GM_CK5805	C 608	11.4	54.3	36	29	TA113E05Q	TA113E05Q
C 536	11.6	55.2	85	14	CD415624	CD415624 GM_CK5805	C 609	11.4	54.3	37	9	AU254721	AU254721
C 537	11.6	55.2	85	28	BH908345	BH908345 SALK 0474	C 610	11.4	54.3	39	28	BH907039	BH907039 SALK 0375
C 538	11.6	55.2	86	9	A1462833	A1462833 vb37d01.x	C 611	11.4	54.3	44	28	BH789203	BH789203 SALK 0009
C 539	11.6	55.2	86	9	A1538919	A1538919 cp75a02.x	C 612	11.4	54.3	44	28	BH789203	BH789203 Arabidops
C 540	11.6	55.2	86	9	A1538919	A1538919 cp75a02.x	C 613	11.4	54.3	46	28	AZ777964	AZ777964 2M0012C23
C 541	11.6	55.2	86	28	BH906369	BH906369 SALK 1097	C 614	11.4	54.3	48	29	BZ595374	BZ595374 SALK 0869
C 542	11.6	55.2	86	28	BH906370	BH906370 SALK 1097	C 615	11.4	54.3	49	9	AU007710	AU007710
C 543	11.6	55.2	86	28	BH906371	BH906371 SALK 1097	C 616	11.4	54.3	50	28	BH636470	BH636470 1008011E0
C 544	11.6	55.2	86	29	DM546313	DM546313 Drosophila	C 617	11.4	54.3	50	9	AU010193	AU010193
C 545	11.6	55.2	87	9	A1597718	A1597718 tuc51h01.x	C 618	11.4	54.3	50	9	AU010386	AU010386
C 546	11.6	55.2	87	9	AV534789	AV534789 AV534789	C 619	11.4	54.3	50	28	BH866406	BH866406 SALK 1012
C 547	11.6	55.2	87	12	BM053015	BM053015	C 620	11.4	54.3	51	29	AL753784	AL753784 Arabidops
C 548	11.6	55.2	87	28	BH851607	BH851607 SALK 0243	C 621	11.4	54.3	52	29	BZ292315	BZ292315 SALK 1237
C 549	11.6	55.2	87	29	BZ660879	BZ660879 SALK 1391	C 622	11.4	54.3	52	29	BZ292316	BZ292316 SALK 1238
C 550	11.6	55.2	88	29	BZ767672	BZ767672 SALK 1294	C 623	11.4	54.3	54	9	AA654697	AA654697 uc73d03.s
C 551	11.6	55.2	88	9	A1406837	A1406837 EST235124	C 624	11.4	54.3	55	9	AL440743	AL440743 sbs3e06.y
C 552	11.6	55.2	89	9	A1523226	A1523226 ar70d07.r	C 625	11.4	54.3	55	9	AA465946	AA465946 v6f6d07.r
C 553	11.6	55.2	89	9	AA442834	AA442834 g3f1l0e.r	C 626	11.4	54.3	57	28	BH636414	BH636414 1008011B1
C 554	11.6	55.2	89	14	CB885113	CB885113 Ma230404a	C 627	11.4	54.3	57	29	AL945826	AL945826 Arabidops
C 555	11.6	55.2	89	29	BZ767670	BZ767670 SALK 1391	C 628	11.4	54.3	58	9	AA508441	AA508441 og78f10.s
C 556	11.6	55.2	90	9	A1656705	A1656705 uc47d12.x	C 629	11.4	54.3	59	9	AL451268	AL451268 uc75c01.x
C 557	11.6	55.2	90	9	AM080543	AM080543 xc24d11.x	C 630	11.4	54.3	60	29	BZ380224	BZ380224 SALK 1148
C 558	11.6	55.2	90	9	AM693694	AM693694 NP668B03S	C 631	11.4	54.3	61	9	AA460636	AA460636 zx62d01.r
C 559	11.6	55.2	91	9	AI020565	AI020565 ua96a08.r	C 632	11.4	54.3	61	14	D18665	D18665 MUSGS01726
C 560	11.6	55.2	91	9	AI086512	AI086512 oz60c08.x	C 633	11.4	54.3	62	9	AM073526	AM073526 x440a03.x
C 561	11.6	55.2	91	9	AU071129	AU071129	C 634	11.4	54.3	62	10	BG099651	BG099651 nag55f01.
C 562	11.6	55.2	91	10	BF9595130	BF9595130 su75d11.Y	C 635	11.4	54.3	63	29	AG265691	AG265691 Lotus Jap
C 563	11.6	55.2	91	10	BF064369	BF064369 SMOVAFCAD	C 636	11.4	54.3	64	10	AM874932	AM874932 SWYACAL04
C 564	11.6	55.2	91	14	D18617	D18617 MUSGS01678	C 637	11.4	54.3	64	12	B1097367	B1097367 SWYACAL04
C 565	11.6	55.2	92	9	AI110529	AI110529 SMOVAFCAD	C 638	11.4	54.3	64	14	C02331	C02331 HDMGS000682
C 566	11.6	55.2	92	14	CB165114	CB165114 44 Al.falt	C 639	11.4	54.3	64	28	BH866366	BH866366 SALK 1012
C 567	11.6	55.2	92	28	BH856181	BH856181 SALK 0832	C 640	11.4	54.3	65	14	T56691	T56691 ya95d07.s2
C 568	11.6	55.2	93	9	AA884587	AA884587 am38d07.s	C 641	11.4	54.3	68	28	BH418348	BH418348 Al-nm22-G
C 569	11.6	55.2	94	9	AA720433	AA720433 SMOVAFCAD	C 642	11.4	54.3	68	28	BH789943	BH789943 SALK 0528
C 570	11.6	55.2	94	29	BZ666241	BZ666241 SMOVAFCAD	C 643	11.4	54.3	68	28	BZ662588	BZ662588 SALK 0260
C 571	11.6	55.2	95	9	AU258004	AU258004	C 644	11.4	54.3	68	29	AA971170	AA971170 op86c05.s
C 572	11.6	55.2	95	13	BUD06520	BUD06520 604151809	C 645	11.4	54.3	69	28	AZ810513	AZ810513 2M0076N01
C 573	11.6	55.2	95	14	H61099	H61099 yf51c12.r1	C 646	11.4	54.3	69	29	BZ584508	BZ584508 3590.1.57
C 574	11.6	55.2	95	14	CA844389	CA844389 JPSSRG 2A	C 647	11.4	54.3	70	13	B0592241	B0592241 E012698-0
C 575	11.6	55.2	95	28	BH864029	BH864029 SALK 0951	C 648	11.4	54.3	71	28	AL757325	AL757325 Arabidops
C 576	11.6	55.2	96	28	BH223697	BH223697 1006114D1	C 649	11.4	54.3	72	28	BH846622	BH846622 SALK 0093
C 577	11.6	55.2	97	9	AL709297	AL709297 ac02a08.x	C 650	11.4	54.3	72	29	BX290034	BX290034 Arabidops
C 578	11.6	55.2	97	9	AL783986	AL783986	C 651	11.4	54.3	73	9	AA754997	AA754997 v775e05.r
C 579	11.6	55.2	98	9	AV963943	AV963943	C 652	11.4	54.3	73	10	AM874908	AM874908 SWYACAL04
C 580	11.6	55.2	98	10	BF632171	BF632171 NF018G06D	C 653	11.4	54.3	73	28	AA050026	AA050026 rdx00003a
C 581	11.6	55.2	98	10	BE042421	BE042421 ho18g01.x	C 654	11.4	54.3	73	29	AL944498	AL944498 Arabidops
C 582	11.6	55.2	98	12	BM984192	BM984192 UT-CF-DX1	C 655	11.4	54.3	74	12	B0066433	B0066433 BJO66433
C 583	11.6	55.2	98	14	CA844389	CA844389 JPSSRG 2A	C 656	11.4	54.3	74	12	BZ290450	BZ290450 SALK 0238
C 584	11.6	55.2	98	14	CA844390	CA844390 JPSSRG 2B	C 657	11.4	54.3	74	29	BX288293	BX288293 Arabidops
C 585	11.6	55.2	98	28	BH632443	BH632443 1007095D0	C 658	11.4	54.3	75	9	AM597097	AM597097 671212.Y
C 586	11.6	55.2	98	28	BH789947	BH789947 SALK 0528	C 659	11.4	54.3	75	9	AA915292	AA915292 v228a03.r
C 587	11.6	55.2	98	28	BZ353365	BZ353365 SALK 1202	C 660	11.4	54.3	76	9	AM059619	AM059619 HUTH.bsst
C 588	11.6	55.2	99	10	BF146464	BF146464 uy29c09.x	C 661	11.4	54.3	76	9	AM059619	AM059619 HUTH.bsst

662	11.4	54.3	76	28	BH866100	SALK_1007	C 735	11.4	54.3	97	29	EX003083
663	11.4	54.3	76	29	AL942915	ArabiDops	C 736	11.4	54.3	98	9	AW466364
664	11.4	54.3	77	28	BH907838	SALK_0443	C 737	11.4	54.3	98	9	AA536938
665	11.4	54.3	77	29	AL771723	ArabiDops	C 738	11.4	54.3	98	10	BG513161
666	11.4	54.3	78	9	AI930938	AI930938 sb44h1.y	C 739	11.4	54.3	98	14	TE60914
667	11.4	54.3	78	14	CD407904	Gm_CK3366	C 740	11.4	54.3	98	28	AF149441
668	11.4	54.3	78	29	CC059730	SALK_0473	C 741	11.4	54.3	98	28	AZ308835
669	11.4	54.3	79	18	BG085632	BG085632 H115F07	C 742	11.4	54.3	98	28	BH813207
670	11.4	54.3	79	28	AZ584347	IM0388014	C 743	11.4	54.3	98	29	CC035140
671	11.4	54.3	79	29	CNS07FEL	AL608619 Anophelies	C 744	11.4	54.3	99	28	BH905685
672	11.4	54.3	80	9	AMS48563	AMS48563 10038E09	C 745	11.4	54.3	99	28	CC035140
673	11.4	54.3	80	28	BH414323	AM597102 sj7b12.y	C 746	11.4	54.3	99	28	BH905426
674	11.4	54.3	81	9	AI521499	BH414323 1007037E0	C 747	11.4	54.3	99	29	BZ663736
675	11.4	54.3	81	28	AZ328092	AZ328092 1M0051M12	C 748	11.4	54.3	100	9	AA063930
676	11.4	54.3	81	29	EX530942	EX530942 ArabiDops	C 749	11.4	54.3	100	9	AI618615
677	11.4	54.3	82	9	AA518895	AA518895 V103902.x	C 750	11.4	54.3	100	10	BP370854
678	11.4	54.3	82	9	AA518895	AA518895 V103902.x	C 751	11.4	54.3	100	10	BE057596
679	11.4	54.3	82	28	BH230418	BH230418 1006157H0	C 752	11.4	54.3	100	10	BE057596
680	11.4	54.3	82	29	AL943645	AL943645 ArabiDops	C 753	11.4	54.3	100	12	BM169322
681	11.4	54.3	83	29	EX287645	EX287645 ArabiDops	C 754	11.4	54.3	100	28	AZ803984
682	11.4	54.3	84	29	BZ592948	SALK_0514	C 755	11.4	54.3	100	28	BH905424
683	11.4	54.3	84	29	BZ592948	SALK_0514	C 756	11.4	54.3	100	28	BH905424
684	11.4	54.3	84	29	BZ592948	SALK_0514	C 757	11.4	54.3	100	28	BH905424
685	11.4	54.3	84	29	BZ592948	SALK_0514	C 758	11.4	54.3	100	29	BZ352958
686	11.4	54.3	84	29	BZ592948	SALK_0514	C 759	11.4	54.3	100	29	BZ352958
687	11.4	54.3	85	9	AA815657	AA815657 ArabiDops	C 760	11.4	54.3	100	29	AL755565
688	11.4	54.3	85	12	BH082759	BH082759 ArabiDops	C 761	11.4	54.3	100	29	AL755565
689	11.4	54.3	85	28	BH411544	BH411544 1007023A0	C 762	11.4	54.3	100	29	AL755565
690	11.4	54.3	85	29	BZ286298	BZ286298 KG08374-3	C 763	11.4	54.3	100	28	AZ803984
691	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 764	11.4	54.3	100	28	BH905424
692	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 765	11.4	54.3	100	28	BH905424
693	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 766	11.4	54.3	100	28	BH905424
694	11.4	54.3	86	29	BZ593586	BZ593586 SALK_0748	C 767	11.4	54.3	100	28	BH905424
695	11.4	54.3	87	9	AI906735	AI906735 ArabiDops	C 768	11.4	54.3	100	29	AL755565
696	11.4	54.3	87	9	AI906735	AI906735 ArabiDops	C 769	11.4	54.3	100	29	AL755565
697	11.4	54.3	87	13	BH212351	BH212351 604159708	C 770	11.4	54.3	100	29	AL755565
698	11.4	54.3	87	28	AZ511968	AZ511968 1M0357E14	C 771	11.4	54.3	100	28	AZ803984
699	11.4	54.3	88	28	AZ511968	AZ511968 1M0357E14	C 772	11.4	54.3	100	28	AZ803984
700	11.4	54.3	89	9	AV950400	AV950400 ArabiDops	C 773	11.4	54.3	100	28	AZ803984
701	11.4	54.3	89	14	LA7027	LA7027 SCRRAP114 3	C 774	11.4	54.3	100	28	AZ803984
702	11.4	54.3	89	28	BH866367	BH866367 SALK_1012	C 775	11.4	54.3	100	28	AZ803984
703	11.4	54.3	90	28	AA909066	AA909066 om12e07.s	C 776	11.4	54.3	100	28	AZ803984
704	11.4	54.3	90	28	BH408816	BH408816 100700990	C 777	11.4	54.3	100	28	AZ803984
705	11.4	54.3	90	29	BZ290897	BZ290897 SALK_0931	C 778	11.4	54.3	100	28	AZ803984
706	11.4	54.3	90	29	BZ290897	BZ290897 SALK_0931	C 779	11.4	54.3	100	28	AZ803984
707	11.4	54.3	90	29	AL767995	AL767995 ArabiDops	C 780	11.4	54.3	100	28	AZ803984
708	11.4	54.3	91	28	AZ809624	AZ809624 2M0073010	C 781	11.4	54.3	100	28	AZ803984
709	11.4	54.3	91	29	BZ290139	BZ290139 SALK_0235	C 782	11.4	54.3	100	28	AZ803984
710	11.4	54.3	91	29	BZ290139	BZ290139 SALK_0235	C 783	11.4	54.3	100	28	AZ803984
711	11.4	54.3	91	29	BZ290139	BZ290139 SALK_0235	C 784	11.4	54.3	100	28	AZ803984
712	11.4	54.3	91	29	BZ290139	BZ290139 SALK_0235	C 785	11.4	54.3	100	28	AZ803984
713	11.4	54.3	92	9	AI871069	AI871069 ArabiDops	C 786	11.4	54.3	100	28	AZ803984
714	11.4	54.3	92	28	BH812709	BH812709 SALK_0555	C 787	11.4	54.3	100	28	AZ803984
715	11.4	54.3	92	28	BH812709	BH812709 SALK_0555	C 788	11.4	54.3	100	28	AZ803984
716	11.4	54.3	92	28	BH812709	BH812709 SALK_0555	C 789	11.4	54.3	100	28	AZ803984
717	11.4	54.3	92	29	CC459173	CC459173 SALK_1256	C 790	11.4	54.3	100	28	AZ803984
718	11.4	54.3	92	29	CC459173	CC459173 SALK_1256	C 791	11.4	54.3	100	28	AZ803984
719	11.4	54.3	93	9	AI134517	AI134517 ArabiDops	C 792	11.4	54.3	100	28	AZ803984
720	11.4	54.3	93	29	BZ292317	BZ292317 SALK_1238	C 793	11.4	54.3	100	28	AZ803984
721	11.4	54.3	94	9	AA512503	AA512503 ArabiDops	C 794	11.4	54.3	100	28	AZ803984
722	11.4	54.3	94	9	AA512503	AA512503 ArabiDops	C 795	11.4	54.3	100	28	AZ803984
723	11.4	54.3	94	29	CC456041	CC456041 ArabiDops	C 796	11.4	54.3	100	28	AZ803984
724	11.4	54.3	94	29	AL938406	AL938406 ArabiDops	C 797	11.4	54.3	100	28	AZ803984
725	11.4	54.3	95	29	BZ593533	BZ593533 SALK_0739	C 798	11.4	54.3	100	28	AZ803984
726	11.4	54.3	95	29	BZ593533	BZ593533 SALK_0739	C 799	11.4	54.3	100	28	AZ803984
727	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 800	11.4	54.3	100	28	AZ803984
728	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 801	11.4	54.3	100	28	AZ803984
729	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 802	11.4	54.3	100	28	AZ803984
730	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 803	11.4	54.3	100	28	AZ803984
731	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 804	11.4	54.3	100	28	AZ803984
732	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 805	11.4	54.3	100	28	AZ803984
733	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 806	11.4	54.3	100	28	AZ803984
734	11.4	54.3	97	28	AA657348	AA657348 nt64a03.s	C 807	11.4	54.3	100	28	AZ803984

C 808	11.2	53.3	62	9	AA601097	AA601097 nos3g01.s	881	11.2	53.3	82	9	AA194434	AA194434 zq04f02.x
809	11.2	53.3	63	29	BZ287519	BZ287519 SALK_0208	882	11.2	53.3	82	12	BM493223	BM493223 EST00006
C 810	11.2	53.3	64	9	AI915515	AI915515 wg30a10.x	883	11.2	53.3	83	28	AZ791578	AZ791578 2M0041K04
C 811	11.2	53.3	64	9	AV560973	AV560973 AV560973	884	11.2	53.3	84	9	AA684263	AA684263 vm68g12.s
C 812	11.2	53.3	64	10	BE228785	BE228785 SMOVL3CAN	885	11.2	53.3	84	28	BH810116	BH810116 SALK_0409
C 813	11.2	53.3	64	13	BQ739121	BQ739121 pt40f01.y	886	11.2	53.3	84	29	BZ663880	BZ663880 SALK_0274
C 814	11.2	53.3	66	9	AA458302	AA458302 sh86a08.y	887	11.2	53.3	85	9	AA060040	AA060040 m391e09.x
C 815	11.2	53.3	66	14	M00056	M00056 TGE8TY74D0	888	11.2	53.3	85	9	AA718968	AA718968 zh20h04.s
C 816	11.2	53.3	66	28	BH643834	BH643834 1008060D1	889	11.2	53.3	85	12	B1317990	B1317990 AV951981
C 817	11.2	53.3	66	29	AL941813	AL941813 Arabidops	890	11.2	53.3	85	9	AA718968	AA718968 zh20h04.s
C 819	11.2	53.3	66	29	BK289557	BK289557 Arabidops	891	11.2	53.3	85	12	B1318004	B1318004 AV951981
C 820	11.2	53.3	67	13	DME545229	DME545229 Drosophil	892	11.2	53.3	85	29	B2354887	B2354887 SALK_1259
C 821	11.2	53.3	67	13	BQ264657	AA269867 va55f10.x	893	11.2	53.3	86	9	AI559341	AI559341 t943h08.x
C 822	11.2	53.3	68	9	AU008270	AA269867 va55f10.x	894	11.2	53.3	86	13	B0865716	B0865716 S057E11.P
C 823	11.2	53.3	68	9	AU008297	AU008270 AUC08270	895	11.2	53.3	86	28	B38049	B38049 HS-1046-B2-
C 824	11.2	53.3	68	9	AA663254	AA663254 hh76c11.y	896	11.2	53.3	87	9	AU012697	AU012697 AUC007704
C 825	11.2	53.3	68	14	CO1004	CO1004 HUMG8000397	897	11.2	53.3	87	9	AU012700	AU012697 AUC007704
C 826	11.2	53.3	68	28	AZ309853	AZ309853 1M0017M08	898	11.2	53.3	87	28	BH186923	BH186923 032.P-09-
C 827	11.2	53.3	68	28	AZ340768	AZ340768 1M0072A14	899	11.2	53.3	87	28	BH609566	BH609566 HIV1B11
C 828	11.2	53.3	69	9	AZ815575	AZ815575 2M0083K20	900	11.2	53.3	87	28	BH857475	BH857475 SALK_0725
C 829	11.2	53.3	69	9	AA582804	AA582804 1BW Neutro	901	11.2	53.3	87	28	BH857478	BH857478 SALK_0725
C 830	11.2	53.3	69	13	BQ758141	BQ758141 Ehma01_SQ	902	11.2	53.3	87	29	B2352527	B2352527 SALK_0809
C 831	11.2	53.3	70	29	AI077347	AI077347 oy65g11.x	903	11.2	53.3	87	29	B2768249	B2768249 SALK_0809
C 832	11.2	53.3	70	29	BZ593095	BZ593095 SALK_0603	904	11.2	53.3	87	29	AL765961	AL765961 Arabidops
C 833	11.2	53.3	70	29	BZ595179	BZ595179 SALK_0862	905	11.2	53.3	87	29	CNS07RAJ	AL765961 Arabidops
C 834	11.2	53.3	71	28	BH847286	BH847286 SALK_0508	906	11.2	53.3	88	9	AA755755	AA755755 sl09a02.y
C 835	11.2	53.3	71	29	BZ595177	AA755029 vv75h08.x	907	11.2	53.3	88	9	AA415019	AA415019 BQ541094
C 836	11.2	53.3	72	9	AA755029	AA755029 vv75h08.x	908	11.2	53.3	88	13	BQ541094	BQ541094 p86cf07.y
C 837	11.2	53.3	72	12	B1937436	B1937436 dd83e10.y	909	11.2	53.3	88	14	CB836236	CB836236 OSTF041E7
C 838	11.2	53.3	72	14	W89090	W89090 zh70h06.x1	910	11.2	53.3	88	14	CB836236	CB836236 OSTF041E7
C 839	11.2	53.3	73	9	AA952424	AA952424 AV952424	911	11.2	53.3	88	14	CB836236	CB836236 OSTF041E7
C 840	11.2	53.3	73	10	BF727501	BF727501 SMOVL3CAN	912	11.2	53.3	88	29	AL7757085	AL7757085 Arabidops
C 841	11.2	53.3	73	10	BE058120	BE058120 sh11f04.y	913	11.2	53.3	89	13	BQ256730	BQ256730 NISC_K005
C 842	11.2	53.3	73	10	BE058120	BE058120 sh11f04.y	914	11.2	53.3	89	13	BQ256730	BQ256730 NISC_K005
C 843	11.2	53.3	73	12	BE420479	BE420479 SMOVL2CAS	915	11.2	53.3	90	13	B0862354	B0862354 S014F01.P
C 844	11.2	53.3	74	28	AZ306924	AZ306924 1M0080N08	916	11.2	53.3	91	9	AA423416	AA423416 ve38h02.x
C 845	11.2	53.3	74	29	AZ582307	AZ582307 1M0374B10	917	11.2	53.3	91	9	AA586853	AA586853 nm67F06.s
C 846	11.2	53.3	74	29	CC458994	CC458994 SALK_1234	918	11.2	53.3	91	28	AZ611942	AZ611942 1M0438P01
C 847	11.2	53.3	75	12	BM256975	BM256975 sak19e09.y	919	11.2	53.3	91	28	BH243886	BH243886 MHA_A02.
C 848	11.2	53.3	75	28	BH891943	BH891943 3526.1.19	920	11.2	53.3	91	28	BH243886	BH243886 MHA_A02.
C 849	11.2	53.3	75	29	AG250570	AG250570 Lotus_fap	921	11.2	53.3	91	28	BH243886	BH243886 MHA_A02.
C 850	11.2	53.3	75	29	CNS025H7	AA182068 Retraodon	922	11.2	53.3	92	9	AA317134	AA317134 sg45b09.y
C 851	11.2	53.3	76	9	AA703311	AA703311 zj11a11.s	923	11.2	53.3	92	9	AA317134	AA317134 sg45b09.y
C 852	11.2	53.3	76	9	AI120991	AI120991 ub75f06.x	924	11.2	53.3	92	12	BM127992	BM127992 PY74e02.y
C 853	11.2	53.3	76	28	AZ566794	AZ566794 226PvE05	925	11.2	53.3	92	12	BM127992	BM127992 PY74e02.y
C 854	11.2	53.3	77	12	BF506946	BF506946 11292P-7	926	11.2	53.3	92	14	BM332592	BM332592 EST00009
C 855	11.2	53.3	77	12	BF506946	BF506946 11292P-7	927	11.2	53.3	93	12	BM332592	BM332592 EST00009
C 856	11.2	53.3	78	10	BF506946	BF506946 11292P-7	928	11.2	53.3	93	14	BM332592	BM332592 EST00009
C 857	11.2	53.3	78	12	BF506946	BF506946 11292P-7	929	11.2	53.3	93	14	BM332592	BM332592 EST00009
C 858	11.2	53.3	78	14	U77315	U77315 HSU77315.Hu	930	11.2	53.3	93	14	BM332592	BM332592 EST00009
C 859	11.2	53.3	78	28	BH909096	BH909096 SALK_0519	931	11.2	53.3	94	9	AI718525	AI718525 as43e07.x
C 860	11.2	53.3	78	28	BH909096	BH909096 SALK_0519	932	11.2	53.3	94	9	AI718525	AI718525 as43e07.x
C 861	11.2	53.3	79	9	AA128193	AA128193 z192a12.x	933	11.2	53.3	94	9	AI718525	AI718525 as43e07.x
C 862	11.2	53.3	79	9	AA128193	AA128193 z192a12.x	934	11.2	53.3	94	9	AI718525	AI718525 as43e07.x
C 863	11.2	53.3	79	9	AU011979	AU011979 AUC011979	935	11.2	53.3	94	10	BG169554	BG169554 UT-M-BH3-
C 864	11.2	53.3	79	10	BF506914	BF506914 1116P-24b	936	11.2	53.3	94	10	BG169554	BG169554 UT-M-BH3-
C 865	11.2	53.3	79	12	BM285360	BM285360 EST00001	937	11.2	53.3	94	10	BG169554	BG169554 UT-M-BH3-
C 866	11.2	53.3	79	12	BM285360	BM285360 EST00001	938	11.2	53.3	95	12	BM285360	BM285360 EST00001
C 867	11.2	53.3	79	13	BM493227	BM493227 EST00010	939	11.2	53.3	95	12	BM285360	BM285360 EST00001
C 868	11.2	53.3	79	14	CA995251	CA995251 g105a08.	940	11.2	53.3	95	28	AZ242093	AZ242093 dae73e01.
C 869	11.2	53.3	79	14	CA995251	CA995251 g105a08.	941	11.2	53.3	96	9	AA208711	AA208711 mae4d05.x
C 870	11.2	53.3	79	28	BH789220	BH789220 SALK_0010	942	11.2	53.3	96	13	BQ593063	BQ593063 S015674-0
C 871	11.2	53.3	79	28	BH789220	BH789220 SALK_0010	943	11.2	53.3	96	29	BZ357430	BZ357430 SALK_1307
C 872	11.2	53.3	80	9	AA908718	AA908718 o101d12.s	944	11.2	53.3	97	9	AA666842	AA666842 vm65f04.s
C 873	11.2	53.3	80	9	AL853232	AL853232 AL853232	945	11.2	53.3	97	9	AA666842	AA666842 vm65f04.s
C 874	11.2	53.3	80	28	BH800359	BH800359 1008124D0	946	11.2	53.3	97	9	AA666842	AA666842 vm65f04.s
C 875	11.2	53.3	80	28	BH800359	BH800359 1008124D0	947	11.2	53.3	97	9	AA666842	AA666842 vm65f04.s
C 876	11.2	53.3	80	29	AL937974	AL937974 Arabidops	948	11.2	53.3	97	9	AA666842	AA666842 vm65f04.s
C 877	11.2	53.3	81	9	AA897750	AA897750 Arabidops	949	11.2	53.3	97	12	BM674282	BM674282 1a08e005.
C 878	11.2	53.3	81	9	AA897750	AA897750 Arabidops	950	11.2	53.3	97	12	BM674282	BM674282 1a08e005.
C 879	11.2	53.3	81	9	AA897750	AA897750 Arabidops	951	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 880	11.2	53.3	81	9	AA897750	AA897750 Arabidops	952	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 881	11.2	53.3	81	9	AA897750	AA897750 Arabidops	953	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 882	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	954	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 883	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	955	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 884	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	956	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 885	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	957	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 886	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	958	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 887	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	959	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 888	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	960	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 889	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	961	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 890	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	962	11.2	53.3	97	28	AZ492227	AZ492227 1M0326B16
C 891	11.2	53.3	82	9	AA659576	AA659576 n63b02.s	963	11.2	53.3	97	28	AZ492227	AZ492227 1



Accession	Length	Score	DB	Length	Score	DB	Length	Score	DB
C 954	11.2	53.3	98	14	CA520780	KS11016H0	CA520780	KS11016H0	CA520780
C 955	11.2	53.3	98	28	AZ592186	IM0402H24	AZ592186	IM0402H24	AZ592186
C 956	11.2	53.3	98	28	BZ663770	SALK_0273	BZ663770	SALK_0273	BZ663770
C 957	11.2	53.3	99	10	BZ248200	NF002G04D	BZ248200	NF002G04D	BZ248200
C 958	11.2	53.3	99	11	CNS0813X	re	CNS0813X	re	CNS0813X
C 959	11.2	53.3	99	12	BM935438	UI-M-BH3-	BM935438	UI-M-BH3-	BM935438
C 960	11.2	53.3	99	13	BQ287277	i165e03.x	BQ287277	i165e03.x	BQ287277
C 961	11.2	53.3	99	29	AL757409	Arbidiops	AL757409	Arbidiops	AL757409
C 962	11.2	53.3	100	9	AA015156	m163a07.r	AA015156	m163a07.r	AA015156
C 963	11.2	53.3	100	9	AM101871	sd71906.y	AM101871	sd71906.y	AM101871
C 964	11.2	53.3	100	9	AM459607	sh89d02.y	AM459607	sh89d02.y	AM459607
C 965	11.2	53.3	100	9	AM582100	MR3-ST019	AM582100	MR3-ST019	AM582100
C 966	11.2	53.3	100	9	AW781526	sl81c04.y	AW781526	sl81c04.y	AW781526
C 967	11.2	53.3	100	10	AA513622	nh29e11.s	AA513622	nh29e11.s	AA513622
C 968	11.2	53.3	100	10	BE151753	QV3-HT030	BE151753	QV3-HT030	BE151753
C 969	11.2	53.3	100	12	BE762761	QV3-NT002	BE762761	QV3-NT002	BE762761
C 970	11.2	53.3	100	12	BM447217	DSA007D11	BM447217	DSA007D11	BM447217
C 971	11.2	53.3	100	12	BM738230	K-EST0002	BM738230	K-EST0002	BM738230
C 972	11.2	53.3	100	13	BM069148	BM069148	BM069148	BM069148	BM069148
C 973	11.2	53.3	100	28	AF087410	AF087410	AF087410	AF087410	AF087410
C 974	11.2	53.3	100	28	CC044689	3591_1.16	CC044689	3591_1.16	CC044689
C 975	11.2	53.3	100	29	CC044746	3591_1.16	CC044746	3591_1.16	CC044746
C 976	11.2	53.3	100	29	CC457081	SALK_1061	CC457081	SALK_1061	CC457081
C 977	11.2	53.3	100	29	EX002146	Arbidiops	EX002146	Arbidiops	EX002146
C 978	11.2	53.3	100	29	AZ581676	IM0370N06	AZ581676	IM0370N06	AZ581676
C 979	11.2	53.3	100	29	TA256C04P	T. brucei	TA256C04P	T. brucei	TA256C04P
C 980	11.2	53.3	100	29	TA83F04Q	AL970990	TA83F04Q	AL970990	TA83F04Q
C 981	11.2	53.3	100	29	AZ759901	IM0553H07	AZ759901	IM0553H07	AZ759901
C 982	11.2	53.3	100	29	BZ352519	SALK_0809	BZ352519	SALK_0809	BZ352519
C 983	11.2	53.3	100	29	BZ352520	SALK_0809	BZ352520	SALK_0809	BZ352520
C 984	11.2	53.3	100	29	BZ352521	SALK_0809	BZ352521	SALK_0809	BZ352521
C 985	11.2	53.3	100	29	BQ584580	B014866	BQ584580	B014866	BQ584580
C 986	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 987	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 988	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 989	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 990	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 991	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 992	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 993	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 994	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 995	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 996	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 997	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 998	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 999	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871
C 1000	11.2	53.3	100	29	AZ321871	IM0042F02	AZ321871	IM0042F02	AZ321871

## ALIGNMENTS

RESULT 1  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AT1218421  
IMAGE:1845595 3', mRNA sequence.

AT1218421  
AT1218421.1 GI:3798236

EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Insert Length: 925 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 73.  
Location/Qualifiers

## FEATURES

source

1..82

/organism="Homo sapiens"

/mol type="mRNA"

/db xref="taxon:9606"

/clone="IMAGE:1845595"

/lab host="DH10B"

/clone lib="Soares\_NFL\_T\_GBC\_S1"

/note="Organ: pooled; Vector: PT73D-Pac (Pharmacia) with  
a modified polylinker; Site: 1: Not 1; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI CGAP CGBI) were mixed, and ss circles were made in  
vivo. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo."

## BASE COUNT

37 a

11 c

13 g

21 t

Query Match 77.1% Score 16.2; DB 9; Length 82;  
Best Local Similarity 85.7% Pred. No. 5.1e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## QY

1

AGATTTCCTAGGAATTCANATC 21

46

AAATTTCCTAGGAATTCANATC 66

## Db

46

AAATTTCCTAGGAATTCANATC 66

## RESULT 2

CA339945

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1

(Bases 1 to 57)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
CDNA Library Preparation:  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL  
DNA Sequencing Center (NISC)  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
Plate: L1AM12449 row: G column: 21  
Seq primer: M13P1 reverse primer (ABI).  
Location/Qualifiers

1..57

/organism="Rattus norvegicus"

/mol type="mRNA"

/db xref="taxon:10116"

/clone="IMAGE:5622956"

/sex="male"

/tissue type="dorsal prostate"

/dev stage="adult, 14 month"

/dev stage="adult, 14 month"



```

/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Pr32"
/Note="Organ: prostate; Vector: pCMV-SPOK6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Constructed by Invitrogen. Note:
this is a NCI CGAP library."
BASE COUNT      15 a      15 c      12 g      15 t
ORIGIN
Query Match      72.4%; Score 15.2; DB 14; Length 57;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 AGATTCTAGGAGATTCAAT 20
Db      29 ACATTCTAGGAGATTCAATT 48

RESULT 3
LOCUS      A2782789      84 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION      2M00023P07R Mouse 10kb plasmid UGCLM library Mus musculus genomic
ACCESSION      A2782789
VERSION      A2782789.1 GI:12916863
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
1 (bases 1 to 84)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0023 row: P column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 84.
Location/Qualifiers
1..84
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCCM0023P07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/Note="Vector: PMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

```

of PMD2 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      24 a      18 c      14 g      28 t
ORIGIN
Query Match      72.4%; Score 15.2; DB 26; Length 84;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 AGATTCTAGGAGATTCAAT 20
Db      23 AGTTTCTAGTAATTCAGAT 42

RESULT 4
LOCUS      CB405258      87 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION      OSTR040A2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION      CB405258
VERSION      CB405258.1 GI:30746985
KEYWORDS      EST.
SOURCE      Caenorhabditis elegans
ORGANISM      Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae
1 (bases 1 to 87)
Reboul,V., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong
C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson
J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jena,S., Chevet,E., Papanicolaou,V., Tolias,P.P.,
Placsek,J., Snyder,M., Huang,R., Chan,M.R., Lee,H.,
Doucette-Stamm,J., Hill,D.R. and Vidal,M.
C. elegans ORFome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
expression
Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@fcl.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact david_hill@fcl.harvard.edu or
marc.vidal@fcl.harvard.edu
POLYA=No.
Location/Qualifiers
1..87
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/Note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pC086"
BASE COUNT      24 a      19 c      19 g      25 t
ORIGIN
Query Match      72.4%; Score 15.2; DB 14; Length 87;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;

```

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GATTTCAGGAATTCAAATC 21  
 Db 41 GATTGCGAGGATTCAGT 60

RESULT 5  
 AL940051/c 91 bp DNA linear GSS 24-OCT-2002  
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-243H10-014396,  
 DEFINITION genomic survey sequence.

ACCESSION AL940051  
 VERSION AL940051.1 GI:24396500  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE 1 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.  
 and Weissshaar, B.  
 A pipeline for automated high-throughput generation of FSTs  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines

JOURNAL 2 Unpublished  
 REFERENCE 3 (bases 1 to 91)  
 AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.  
 TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 for flanking sequence tag based reverse genetics  
 JOURNAL Unpublished

REFERENCE 3 (bases 1 to 91)  
 AUTHORS Rosso, M., Strizhov, N., Li, Y. and Weissshaar, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-OCT-2002) Weissshaar B. Max-Planck-Institut fuer  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence is recovered from the left border of the T-DNA. It  
 indicates an insertion within the locus defined by clone F1809. The  
 sequences are generated at the MPI for Plant Breeding Research in  
 the context of the GABI-Kat project. GABI-Kat is part of the German  
 plant Genomics program designated 'GABI'. Information on line  
 availability can be found at:  
 http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES  
 source Location/Qualifiers

1..91  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone\_lib="GK-243H10-014396"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAC161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were  
 processed for submission. T-DNA derived sequences were  
 removed"

BASE COUNT 35 a 19 c 9 g 28 t  
 ORIGIN

Query Match 72.4%; Score 15.2; DB 29; Length 91;  
 Best Local Similarity 85.0%; Pred. No. 1.5e+04;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTTCAGGAATTCAAAT 20  
 Db 67 AGTTTCGAGGATTCAGT 48

RESULT 6  
 BU837156/c 93 bp mRNA linear EST 15-OCT-2002  
 LOCUS T095D05 Populus apical shoot cDNA library Populus tremula x Populus  
 DEFINITION tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION BU837156  
 VERSION BU837156.1 GI:24019968  
 KEYWORDS EST.

SOURCE Populus tremula x Populus tremuloides  
 ORGANISM Populus tremula x Populus tremuloides  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 93)  
 AUTHORS Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags  
 from multiple libraries

JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES  
 source Location/Qualifiers

1..93  
 /organism="Populus tremula x Populus tremuloides"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:47664"  
 /tissue\_type="apical shoot"  
 /clone\_lib="Populus apical shoot cDNA library"

BASE COUNT 32 a 13 c 16 g 32 t  
 ORIGIN  
 Query Match 72.4%; Score 15.2; DB 13; Length 93;  
 Best Local Similarity 85.0%; Pred. No. 1.5e+04;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTTCAGGAATTCAAAT 20  
 Db 58 AGATTTCAGGAATTCAAAT 39

RESULT 7  
 BU890262/c 97 bp mRNA linear EST 17-OCT-2002  
 LOCUS P034B05 Populus petioles cDNA library Populus tremula cDNA 5 prime,  
 DEFINITION mRNA sequence.

ACCESSION BU890262  
 VERSION BU890262.1 GI:24101327  
 KEYWORDS EST.

SOURCE Populus tremula  
 ORGANISM Populus tremula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE 1 (bases 1 to 97)  
 AUTHORS Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags  
 from multiple libraries

JOURNAL Unpublished  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES  
 source Location/Qualifiers

1..97  
 /organism="Populus tremula"  
 /mol\_type="mRNA"

/db xref="taxon:113636"  
/tissue\_type="petioles"  
/clone\_lib="Populus petioles cDNA library"  
BASE COUNT 35 a 16 c 14 g 32 t  
ORIGIN

Query Match 72.4%; Score 15.2; DB 13; Length 97;  
Best Local Similarity 85.0%; Pred. No. 1.5e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATCAAT 20  
60 AGATTGAGAGATTCAT 41

RESULT 8 AA749115 73 bp mRNA linear EST 27-JAN-1998  
LOCUS 058604.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1309206 3',  
DEFINITION mRNA sequence.  
ACCESSION AA749115 GI:2789073  
VERSION AA749115.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 73)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-rt@mail.nih.gov](mailto:cgapbs-rt@mail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
found through the I.M.A.G.E.B. Consortium/LINM at:  
[www-bio.linn.gov/bbrp/image/image.html](http://www-bio.linn.gov/bbrp/image/image.html)  
Insert Length: 805 Std Error: 0.00  
Seq Primer: -40m13 fwd. ET from Amerham  
High quality sequence stop: 65.

FEATURES  
source  
Location/Qualifiers  
1..73

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1309206"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_GCB1"

/note="Vector: pUT3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCGAAGTGGACGCGCCGTCATTTTCTTTTCTTT-3',  
(Pharmacia), digested with Not I and Eco RI adaptors  
and Eco RI sites of the modified pUT3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 29 a 10 c 7 g 27 t  
ORIGIN

Y Match 69.5%; Score 14.6; DB 9; Length 73;  
Local Similarity 81.0%; Pred. No. 2.7e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 AGATTCTAGGAATCAATC 21  
17 AGATTGAGAGATTCATC 37

RESULT 9 BZ593365 93 bp DNA linear GSS 07-JAN-2003  
LOCUS SALK\_070370.34.05.n Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_070370.34.05.n, genomic  
survey sequence.  
ACCESSION BZ593365 GI:27533884  
VERSION BZ593365  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE Alonso J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgilab  
, C., Jeske, A., Karnes, M., Kim, C.U., Parker, H., Prednis, L., Shinn, P.,  
, Zimmermann, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished

JOURNAL Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: [eckers@salk.edu](mailto:eckers@salk.edu)  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.

FEATURES  
source  
Location/Qualifiers  
1..93

/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_070370.34.05.n"  
/note="PCR was performed on Arabidopsis thaliana lines  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"  
BASE COUNT 31 a 12 c 16 g 34 t  
ORIGIN

Query Match 69.5%; Score 14.6; DB 29; Length 93;  
Best Local Similarity 81.0%; Pred. No. 2.8e+04;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATCAATC 21  
10 AGATTGAGAGATTCATC 30

RESULT 10 AM695026 63 bp mRNA linear EST 21-DEC-2000  
LOCUS NF082E06ST1F1050 Developing stem Medicago truncatula cDNA clone  
DEFINITION NF082E06ST 5', mRNA sequence.  
ACCESSION AM695026  
VERSION AM695026.2 GI:11957373  
KEYWORDS EST.  
SOURCE Medicago truncatula (barrel medic)

```

ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE
1 (bases 1 to 63)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,T.T., Weller,T.W., May,G.D. and Dixon
,R.A.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
Unpublished
On Apr 14, 2000 this sequence version replaced gi:7569788.

JOURNAL
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 685 Std Error: 0.00
Plate: 082 Row: E Column: 06
Seq primer: TCACACAGAGAACGCTATGAC.

FEATURES
source
1..63
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF082E065T"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/clone_lib="Developing stem"
/notes="Vector: lambda zap; Contains a mixture of
internodal stem segments"

BASE COUNT
31 a 16 c 5 g 11 t

ORIGIN
5 TTCTAGGAATTCAAAT 20
30 TTGTAGGAATTCAAAT 15

Query Match 68.6%; Score 14.4; DB 9; Length 63;
Best Local Similarity 93.8%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TTCTAGGAATTCAAAT 20
30 TTGTAGGAATTCAAAT 15

RESULT 11
CA513671/c 93 bp mRNA EST 15-NOV-2002
LOCUS 10-3_1H2 Porcine testis phage library Sus scrofa cDNA clone
DEFINITION 10-3_1H2, mRNA sequence.
ACCESSION CA513671
VERSION CA513671.1 GI:25014228
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
1 (bases 1 to 93)
Burkin,H.R., Vieira,A.P. and Miller,D.J.
Direct submission (Burkin, Vieira, Miller)

JOURNAL
Unpublished
Contact: Burkin HR
University of Illinois at Urbana-Champaign
1207 W Gregory Dr, Urbana, IL 61801, USA
Tel: 217 244 5144
Fax: 217 333 8286
Email: burkin@uiuc.edu
Insert Length: 93 Std Error: 0.00
Plate: 10-3_1 Row: H Column: 2
High quality sequence stop: 93.

FEATURES
source
1..93
Location/Qualifiers

```

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="10-3_1H2"
/sex="male"
/lab_host="BLT5616"
/clone_1b="Porcine testis phase library"
/note="Organ: testis; Vector: T7 bacteriophage; Site_1: Eco RI; Site_2: HindIII"
Eco RI: Site_2: HindIII"
23 a 24 c 17 g 29 t

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 68.6%; Score 14.4; DB 14; Length 93;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 AGATTCTAGGATTC 16
|||||
16 AGACTTCTAGGATTC 1

RESULT 12
LOCUS AZ437380 97 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0225B12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0225B12 R, genomic survey sequence.
ACCESSION AZ437380
VERSION AZ437380.1 GI:10561393
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 97)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: B column: 12
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 97.
Location/Qualifiers
1. 97
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0225B12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_1b="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adapter oligonucleotides were
ligated to the blunt ends in high molar excess. The

```

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1/4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 33 a 13 c 19 g 32 t

ORIGIN

Query Match 68.6%; Score 14.4; DB 28; Length 97;  
Best Local Similarity 93.8%; Pred. No. 3.4e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTCTTAGAATTCATA 19  
21 TTCTTAGAATTCATA 36

RESULT 13  
LOCUS BH851999  
DEFINITION BH851999 48 bp DNA linear GSS 13-JUN-2002  
Arabidopsis thaliana genomic clone SALK\_074019.36.90.x, genomic survey sequence.

ACCESSION BH851999  
VERSION BH851999.1 GI:21422870  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriah,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,D.R.  
AUTHORS A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

TITLE Arabidopsis Genome  
JOURNAL Unpublished  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At5g16310 and 300 bases of the 5' end of At5g16320.  
Class: TDNA tagged.

FEATURES  
source location/Qualifiers

1..48  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_074019.36.90.x"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

BASE COUNT 12 a 4 c 12 g 20 t

ORIGIN

Query Match 67.6%; Score 14.2; DB 28; Length 48;  
Local Similarity 84.2%; Pred. No. 3.8e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GATTTCAGAAATTCAAAT 20  
28 GATTTCAGAAATTCAAAT 46

RESULT 14  
LOCUS BG153679/c  
DEFINITION BG153679 60 bp mRNA linear EST 05-FEB-2001  
nags8608.x1 NCI\_CGAP\_Co26 Homo sapiens cDNA IMAGE:4225743 3', mRNA sequence.

ACCESSION BG153679  
VERSION BG153679.1 GI:12665709  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 60)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LINL  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: [info@image.lnl.gov](mailto:info@image.lnl.gov)  
Seq primer: -40UP from Gibco.

FEATURES  
source location/Qualifiers

1..60  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4225743"  
/tissue\_type="normal colonic mucosa"  
/lab\_host="DH10B"  
/clone\_id="NCI\_CGAP Co26"  
/note="Organ: colon; Vector: PAMPI; mRNA made from normal colonic mucosa, cDNA made by oligo-dt priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA library preparation: David B. Krizman, Ph.D.  
Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 17 a 17 c 9 g 17 t

ORIGIN

Query Match 67.6%; Score 14.2; DB 10; Length 60;  
Best Local Similarity 84.2%; Pred. No. 3.9e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GATTTCAGAAATTCAAAT 20  
20 GATTTCAGAAATTCAAAT 2

RESULT 15  
LOCUS AI966296  
DEFINITION AI966296 83 bp mRNA linear EST 30-NOV-2001  
sc36h04.y1 Gm-c1014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1014-1232 5', mRNA sequence.

ACCESSION AI966296  
VERSION AI966296.1 GI:5760933  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE  
AUTHORS  
Shoemaker, R., Keim, P., Vodkin, L., Expelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE  
JOURNAL  
COMMENT  
Public Soybean EST Project  
Unpublished  
Contact: Shoemaker R./Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35601 For further information call: (800)-533-4363 or contact via email: csh@resgen.com  
Seq primer: -40RP from Gibco.

FEATURES  
source  
1..83  
/organism="Glycine max"  
/mol\_type="mRNA"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl014-1232"  
/tissue\_type="leaves, 2-3 week old seedlings, greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl014"  
/note="Vector: pT73Pac (pT73, Pharmacia); Site 1: EcoRI; Site 2: HindIII. This cDNA library was constructed from mRNA isolated from leaves of 2-3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly (dT) primer. EcoRI adapters followed by ligated to the blunt-ended cDNA fragments were digested with EcoRI and HindIII. The cDNA fragments were directionally cloned into the EcoRI-HindIII restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Expelding."

BASE COUNT  
32 a 9 c 8 g 34 t

ORIGIN  
Query Match 67.6%; Score 14.2; DB 9; Length 83;  
Best Local Similarity 84.2%; Pred. No. 4.1e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAAATCAAA 19  
12 AAATTCAAGGAATTCGAA 30

Db

RESULT 16  
BU077154/c 47 bp mRNA linear EST 11-DEC-2001  
LOCUS BU077154 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone X1060a15 3', mRNA sequence.  
DEFINITION  
ACCESSION BU077154 GI:17522070  
VERSION BU077154  
KEYWORDS EST.  
Xenopus laevis (African clawed frog)  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.  
REFERENCE 1 (bases 1 to 47)  
Kikayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.  
Expressed genes in X. laevis embryo

JOURNAL  
COMMENT  
Unpublished  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6855  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.

FEATURES  
source  
1..47  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="X1060a15"  
/tissue\_type="whole embryo"  
/dev stage="stage 25"  
/clone\_lib="NIBB Mochii normalized Xenopus tailbud library"

BASE COUNT  
9 a 3 c 9 g 22 t 4 others

ORIGIN  
Query Match 65.7%; Score 13.8; DB 12; Length 47;  
Best Local Similarity 88.2%; Pred. No. 5.7e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAAATCAAA 19  
19 AGTTCTAGGAAATCAAA 3

Db

RESULT 17  
AA422541 49 bp mRNA linear EST 16-OCT-1997  
LOCUS AA422541  
DEFINITION V614C03.s1 Knowles Solter mouse unfertilized egg Mus musculus cDNA clone IMAGE:835684 5', mRNA sequence.  
ACCESSION AA422541 GI:2101361  
VERSION AA422541  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 49)  
Marra, M., Hillier, L., Allen, M., Bowers, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through INLM; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:495900  
Seq primer: -40m13 fwd, RT from Amersham.

FEATURES  
source  
1..49  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAGE:835684"  
/tissue\_type="unfertilized egg"  
/lab\_host="DH10B"  
/clone\_lib="Knowles Solter mouse unfertilized egg"  
/note="Organ: unfertilized egg; Vector: pBluescribe (modified); Site 1: Mui; Site 2: SalI; Cloned

unidirectionally from mRNA prepared from 5000 unfertilized eggs. Primer: SalI(dT):  
 5'-CGTCGACCGCGACCGTCTTTTCTTTT-3'. cDNAs were  
 cloned into the MluI/SalI sites of a modified pBluescribe  
 vector using commercial linkers (NEB). Average insert  
 size: 1.0 kb."

BASE COUNT 22 a 3 c 10 g 14 t

ORIGIN

Query Match 65.7%; Score 13.8; DB 9; Length 49;  
 Best Local Similarity 88.2%; Pred. No. 5.8e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTCTAGGAATTCAAA 19  
 1 |||||  
 29 AGTCTAGGAATTCAAA 45

RESULT 18  
 AZ810918/c

LOCUS 69 bp DNA linear GSS 20-FEB-2001  
 DEFINITION 2M0076K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0076K14 R, genomic survey sequence.

ACCESSION  
 AZ810918  
 VERSION  
 AZ810918.1 GI:12978657  
 KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0076 row: K column: 14  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 69.  
 Location/Qualifiers  
 1. 69

FEATURES

source

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0076K14"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative

BASE COUNT 21 a 16 c 10 g 22 t

ORIGIN

Query Match 65.7%; Score 13.8; DB 28; Length 69;  
 Best Local Similarity 88.2%; Pred. No. 6.1e+04;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTCTAGGAATTCAAAT 20  
 1 |||||  
 27 TTCTAGGAATTCAAAT 11

RESULT 19  
 AZ956832/c

LOCUS 69 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0223C05R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0223C05 R, genomic survey sequence.

ACCESSION  
 AZ956832  
 VERSION  
 AZ956832.1 GI:13828059  
 KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0223 row: C column: 05  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 69.  
 Location/Qualifiers  
 1. 69

FEATURES

source

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0223C05"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1lb="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 18 a 19 c 11 g 21 t

Query Match 65.7%; Score 13.8; DB 28; Length 69;  
Best Local Similarity 88.2%; Pred. No. 6.1e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGATTCTAGGAATTCGA 17  
18 AGATTCTAGGAATTCGA 2

RESULT 20  
BG153467/c 76 bp mRNA linear EST 05-FEB-2001  
LOCUS nag99a01.x1 NCI\_CGAP\_Co29 Homo sapiens cDNA clone IMAGE:4204320 3',  
DEFINITION mRNA sequence.  
ACCESSION BG153467 GI:12665497  
VERSION BG153467  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 76)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished

JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov

CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

FEATURES  
Source  
1..76  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4204320"  
/tissue\_type="tubulovillous adenoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Co29"  
/note="Organ: colon; Vector: PAMPI; mRNA made from colonic adenoma, cDNA made by oligo-dt priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 22 a 20 c 14 g 20 t

Query Match 65.7%; Score 13.8; DB 10; Length 76;  
Best Local Similarity 88.2%; Pred. No. 6.2e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTCTAGGAATTCGA 18  
24 GATTCTAGGAATTCGA 8

RESULT 21  
BG151684 82 bp mRNA linear EST 05-FEB-2001  
LOCUS nag63b11.x1 NCI\_CGAP\_Co26 Homo sapiens cDNA clone IMAGE:4226252 3',  
DEFINITION mRNA sequence.  
ACCESSION BG151684 GI:12663714  
VERSION BG151684  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 82)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished

JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

FEATURES  
Source  
1..82  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4226252"  
/tissue\_type="normal colonic mucosa"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP Co26"  
/note="Organ: colon; Vector: PAMPI; mRNA made from normal colonic mucosa, cDNA made by oligo-dt priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 22 a 21 c 14 g 24 t 1 others

Query Match 65.7%; Score 13.8; DB 10; Length 82;  
Best Local Similarity 88.2%; Pred. No. 6.2e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GATTCTAGGAATTCGA 18  
40 GATTCTAGGAATTCGA 24

RESULT 22  
BG151856 88 bp mRNA linear EST 05-FEB-2001  
LOCUS nag65d05.x1 NCI\_CGAP\_Co26 Homo sapiens cDNA clone IMAGE:4226360 3',  
DEFINITION mRNA sequence.  
ACCESSION BG151856 GI:12663886  
VERSION BG151856  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 88)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished

JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov



CDNA Library Preparation: David B. Krizman, Ph.D.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:  
 info@image.llnl.gov  
 Seq primer: -40UP from Gibco.

#### FEATURES

Location/Qualifiers

1..88

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:426360"

/tissue\_type="normal colonic mucosa"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Co26"

/note="Organ: colon; Vector: pAMP1, mRNA made from normal

colonic mucosa, cDNA made by oligo-dT priming.

Directionally cloned into UDG sites. Size selected on

agarose gel, average insert size 300 bp. Primary library.

CDNA Library Preparation: David B. Krizman, Ph.D.

Reference: Krizman et al. (1996) Cancer Research

56:5380-5383."

#### BASE COUNT

23 a 23 c 17 g 25 t

#### Query Match

Best Local Similarity 88.2%; Score 13.8; DB 10; Length 88;

#### Matches

15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

#### Db

2 GATTCTAGGAATTCAA 18

35 GAATTCGAGCAATTCAA 19

#### RESULT 23

EX533932

#### LOCUS

88 bp DNA linear GSS 03-JUN-2003

#### DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-505B08-019718,

#### ACCESSION

EX533932

#### VERSION

GSS

#### KEYWORDS

Arabidopsis thaliana (thale cress)

#### SOURCE

Arabidopsis thaliana

#### ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

#### REFERENCE

1. Strizhov, N., Li, Y., Rosso, M., Viehovec, P., Dekker, K., Saedler, H.

#### AUTHORS

and Weishaar, B.

#### TITLE

A pipeline for automated high-throughput generation of ESTs

#### JOURNAL

(flanking sequence tags) from Arabidopsis thaliana T-DNA

#### REFERENCE

2. Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.

#### AUTHORS

A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

#### TITLE

for flanking sequence tag based reverse genetics

#### JOURNAL

Unpublished

#### REFERENCE

3. (bases 1 to 88)

#### AUTHORS

Strizhov, N., Li, Y., Rosso, M. and Weishaar, B.

#### TITLE

Submitted (02-JUN-2003) Weishaar B., Max-Planck-Institut fuer

#### JOURNAL

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

#### COMMENT

This sequence is recovered from the left border of the T-DNA. It

#### FEATURES

indicates an insertion within the locus defined by clone F219. The

#### Location/Qualifiers

sequences are generated at the MPI for Plant Breeding Research in

#### Location/Qualifiers

plant Genetics program designated 'GABI'. Information on line

#### Location/Qualifiers

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

#### source

1..88

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-505B08-019718"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector PAC161. The lines contain one or more T-DNA

insertions. The DNA fragment(s) resulting from the PCR

were directly sequenced to determine the genomic sequence

flanking the insertion. Sequences displaying significant

similarity to the A. thaliana nuclear genome sequence were

processed for submission. T-DNA derived sequences were

removed"

#### BASE COUNT

30 a 12 c 16 g 30 t

#### Query Match

Best Local Similarity 88.2%; Score 13.8; DB 29; Length 88;

#### Matches

15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

#### Db

2 GATTCTAGGAATTCAA 18

43 GATTCTAGGAATTCAA 59

#### RESULT 24

CD028826/c

#### LOCUS

91 bp mRNA linear EST 07-MAY-2003

#### DEFINITION

mgmy001x18f.b Magnaporthe grisea MY Uni-Zap XR library Magnaporthe

#### ACCESSION

CD028826

#### VERSION

EST

#### KEYWORDS

Magnaporthe grisea (anamorph: Pyricularia grisea)

#### SOURCE

Magnaporthe grisea

#### ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

#### REFERENCE

1. (bases 1 to 91)

#### AUTHORS

Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatte, R.

#### TITLE

Expressed sequence tags from the rice blast fungus, Magnaporthe

#### JOURNAL

grisea

#### COMMENT

Unpublished

#### CONTACT

Contact: Ebbole DJ

#### DEPARTMENT

Department of Plant Pathology & Microbiology

#### TEXAS A&M UNIVERSITY

Peterson Bldg, MS2132, College Station, TX 77843-2132, USA

#### TEL

Tel: 979 845 4831

#### FAX

Fax: 979 845 6483

#### EMAIL

Email: d-ebbole@tamu.edu

#### CHROMATOGRAM

Chromatogram file of this sequence is available, see contact person

#### PCR PRIMERS

FORWARD: T3 primer

#### BACKWARD

BACKWARD: T7 primer

#### PLATE

Plate: mgmy001 row: J column: 18

#### SEQ PRIMER

Seq primer: T3

#### Location/Qualifiers

1..91

#### organism

/organism="Magnaporthe grisea"

#### mol\_type

/mol\_type="mRNA"

#### strain

/strain="70-15"

#### db\_xref

/db\_xref="taxon:148305"

#### clone

/clone="mgmy001x18"

#### sex

/sex="Mat1-2 hermaphrodite"

#### cell\_type

/cell\_type="mycelium"

#### clone\_lib

/clone\_lib="Magnaporthe grisea MY Uni-Zap XR library"

#### note

/note="Vector: pBluescriptSK+; Site 1: EcoRI; Site 2: XhoI

#### predominantly

predominantly 5' reads. T7 primer on XhoI side of insert.

Minimal medium mycelium library. Sequences were processed by one of two methods. Where a full-length alignment to the *M. grisea* genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

BASE COUNT 43 a 13 c 19 g 16 t

Query Match 65.7%; Score 13.8; DB 14; Length 91;  
Best Local Similarity 88.2%; Pred. No. 6.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTTCTAGGAATTCAAA 19  
Db 37 ATTCTAGGAATTCATA 21

RESULT 25  
AF087391 91 bp DNA linear GSS 18-APR-2000  
LOCUS AF087391 Chlamydia trachomatis L2 Chlamydia trachomatis genomic  
DEFINITION clone 830 similar to RAD1 protein, genomic survey sequence.  
ACCESSION AF087391 GI:7593958  
VERSION AF087391.1  
KEYWORDS GSS.  
SOURCE Chlamydia trachomatis  
ORGANISM Chlamydia trachomatis  
REFERENCE 1 (bases 1 to 91)  
AUTHORS Wang, L., Steenburg, S.D., Zheng, Y. and Larsen, S.H.  
TITLE Gene identification of Chlamydia trachomatis by random DNA sequencing  
JOURNAL Unpublished  
COMMENT Contact: Wang L.  
Department of Microbiology & Immunology  
Indiana University School of Medicine  
635 Barnhill Drive, MS 255, Indianapolis, IN 46202, USA  
Class: shogun.

FEATURES  
source location/Qualifiers  
1. 91  
/organism="Chlamydia trachomatis"  
/mol\_type="genomic DNA"  
/strain="L2"  
/db\_xref="taxon:813"  
/clone\_1lb="Chlamydia trachomatis L2"  
/note="isolate=4348"  
BASE COUNT 33 a 18 c 11 g 29 t

Query Match 65.7%; Score 13.8; DB 28; Length 91;  
Best Local Similarity 88.2%; Pred. No. 6.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATTC 17  
Db 60 AGATTCTAGGAATACA 76

RESULT 26  
BH758017 91 bp DNA linear GSS 01-MAR-2002  
LOCUS BH758017  
DEFINITION SALK 013098.27.85.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_013098.27.85.x, genomic  
survey sequence.  
ACCESSION BH758017  
VERSION BH758017.1 GI:19042773  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

# REFERENCE

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Kairns, M., Kim, C.T., Parker, H., Prednis, L., Shim, P., Zimmerman, J., and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At5g04410 and 300 bases of the 3' end of At5g04420.  
Class: TDNA tagged.

# JOURNAL

Unpublished  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of At5g04410 and 300 bases of the 3' end of At5g04420.  
Class: TDNA tagged.

# FEATURES

source location/Qualifiers  
1. 91  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_1lb="SALK 013098.27.85.x"  
/note="T-DNA was performed on Arabidopsis thaliana lines each of which contains one or more T-DNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tDNA\\_protocols.html](http://signal.salk.edu/tDNA_protocols.html)"  
BASE COUNT 34 a 12 c 18 g 27 t

Query Match 65.7%; Score 13.8; DB 28; Length 91;  
Best Local Similarity 88.2%; Pred. No. 6.3e+04;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTTCTAGGAATTCAAA 19  
Db 51 ATTCTAGGAATTCATA 67

RESULT 27  
BH615007 48 bp DNA linear GSS 28-JAN-2002  
LOCUS BH615007  
DEFINITION BG00015-3prime Drosophila melanogaster P[GT1] P element insertion  
lines Drosophila melanogaster genomic sequence recovered from 3' end of P element, genomic survey sequence.  
ACCESSION BH615007  
VERSION BH615007.1 GI:18379695  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Lewis, R., Hoskins, R., Liao, G., Mozdén, N., Tsang, G., He, Y., Karpen, G., Bellen, H., Rubin, G., and Spradling, A.  
The Berkeley Drosophila Genome Project Gene Disruption Project  
Unpublished  
Contact: Gerald Rubin  
Berkeley Drosophila Genome Project  
University of California, Berkeley  
LSA Building, Berkeley, CA 94720-3200, USA  
Fax: 5106439947  
Email: getty@fruitfly.berkeley.edu  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of P

element  
The P element insertion position is base 1 in the 48 bases. This insertion position refers to the first base of the 8 base target recognition sequence.  
Class: transposon-tagged.

FEATURES  
source Location/Qualifiers

1..48  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="Drosophila melanogaster P[GT1] P element insertion lines"  
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains one or more P[GT1] P-element transposon insertion. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://www.fruitfly.org/about/methods/inverse.pcr.html>."

BASE COUNT  
17 a 5 c 10 g 16 t

Query Match 64.8%; Score 13.6; DB 28; Length 48;  
Best Local Similarity 80.0%; Pred. No. 7.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAAATCAAT 20  
|||||  
6 AGATTGATGGAAATTAAT 25

Db

RESULT 28  
LOCUS BF789276 50 bp mRNA linear EST 12-JAN-2001  
DEFINITION 602105183F1 NCI CGAP\_Kid14 Mus musculus cDNA clone IMAGE:4223229  
5', mRNA sequence.  
ACCESSION BF789276  
VERSION BF789276.1 GI:12094312  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 50)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNI)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNI at: <http://image.llnl.gov>  
Plate: LILNI9811 row: e column: 22  
High quality sequence stop: 30.  
Location/Qualifiers

FEATURES  
source

1..50  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4223229"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NCI CGAP\_Kid14"  
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library. |"  
BASE COUNT  
19 a 7 c 9 g 15 t

BASE COUNT  
ORIGIN

Query Match 64.8%; Score 13.6; DB 10; Length 50;  
Best Local Similarity 80.0%; Pred. No. 7.1e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAAATCAAT 20  
|||||  
15 AAATTCTAGGAAATCTTAT 34

Db

RESULT 29  
LOCUS BF463652/c 63 bp mRNA linear EST 04-DEC-2000  
DEFINITION BF463652/c  
UI-M-CG0p-bmp-a-11-0-UI.s1 NIH BMAP\_Ret4\_S2 Mus musculus cDNA clone  
UI-M-CG0p-bmp-a-11-0-UI 3', mRNA sequence.  
ACCESSION BF463652  
VERSION BF463652.1 GI:11532835  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 63)  
Normalization and subtraction: two approaches to facilitate gene discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: [MESt@mail.nih.gov](mailto:MESt@mail.nih.gov)

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the retina tissue cDNA library Preparation: M.B. Soares lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements The following repetitive elements were found in this cDNA sequence: 15-105, >B2#SINE/B2  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1..63  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-CG0p-bmp-a-11-0-UI"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH BMAP\_Ret4\_S2"  
/note="Vector: pRTT-D-Pac (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH\_BMAP\_Ret4\_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at [brainest.eng.uowa.edu](http://brainest.eng.uowa.edu). The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine  
TAG\_LIB=NIH\_BMAP\_Ret4\_S2  
TAG\_TISSUE=adult-retina  
TAG\_SEQ=GTGAGCGCCGCC"  
BASE COUNT  
13 a 20 c 13 g 17 t

BASE COUNT  
ORIGIN

Query Match 64.8%; Score 13.6; DB 10; Length 63;  
 Best Local Similarity 80.0%; Pred. No. 7.4e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GATTCTAGGAATCAATC 21  
 38 GATTGCTAGGAATCAATC 19

RESULT 30  
 BG668331/c 71 bp mRNA linear EST 30-APR-2001  
 LOCUS DRACCH10 Rat DRG library Rattus norvegicus cDNA clone DRACCH10 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG668331 GI:13890253  
 VERSION BG668331  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus (Norway rat);  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 71)  
 Xiao H.S., Huang Q.H., Zhang F.X., Bao L., Lu Y.J., Guo C., Yang L.,  
 Huang W.J., Fu G., Xu S.H., Cheng X.P., Yan Q., Zhu Z.D., Zhang  
 X., Chen Z., Han Z.G. and Zhang X.  
 Identification of gene expression profile of dorsal root ganglion  
 in the rat peripheral axotomy model of neuropathic pain  
 Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
 22056133  
 MEDLINE  
 PUBMED 12060780  
 COMMENT Contact: Zhang Xu  
 Laboratory of Sensory System  
 Institute of Neuroscience  
 320 Yue Yang Road, Shanghai 200031, P.R. China  
 Tel: 86-21-64748700-121  
 Fax: 86-21-64713446  
 Email: xu.zhang@ion.ac.cn  
 This clone is also available at Chinese National Human Genome  
 Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
 Pudong New Area, P.R. China. Please contact with Zhang Xu  
 (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)  
 PCR Primers  
 FORWARD: T3  
 BACKWARD: T7  
 Seq primer: T3  
 POLYA=No.

FEATURES  
 source Location/Qualifiers  
 1..71  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="DRACCH10"  
 /sex="male"  
 /tissue\_type="dorsal root ganglion"  
 /dev\_stage="adult"  
 /clone\_lib="Rat DRG library"  
 16 c 22 g 16 t

BASE COUNT 17 a 16 c 22 g 16 t  
 ORIGIN

Query Match 64.8%; Score 13.6; DB 10; Length 71;  
 Best Local Similarity 80.0%; Pred. No. 7.5e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATCAAT 20  
 61 AGGTCTCTGGGAATTCAGAT 42

RESULT 31  
 BU890627

LOCUS BU890627 81 bp mRNA linear EST 17-OCT-2002  
 DEFINITION P039E04 Populus petiolaris cDNA library Populus tremula cDNA 5 prime,  
 mRNA sequence.  
 ACCESSION BU890627 GI:24101692  
 VERSION BU890627.1  
 KEYWORDS EST.  
 SOURCE Populus tremula  
 ORGANISM Populus tremula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids I; Malpighiales; Salicaceae; Populus.  
 1 (bases 1 to 81)  
 Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 The poplar tree transcriptome: Analysis of expressed sequence tags  
 from multiple libraries  
 Unpublished  
 JOURNAL Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES  
 source Location/Qualifiers  
 1..81  
 /organism="Populus tremula"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:113636"  
 /tissue\_type="petioles"  
 /clone\_lib="Populus petiolaris cDNA library"  
 16 a 24 c 20 g 21 t

BASE COUNT 16 a 24 c 20 g 21 t  
 ORIGIN

Query Match 64.8%; Score 13.6; DB 13; Length 81;  
 Best Local Similarity 80.0%; Pred. No. 7.7e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGATTCTAGGAATCAAT 20  
 28 AGATCTCTAGCCACTCAAT 47

RESULT 32  
 AA863156 86 bp mRNA linear EST 29-APR-1998  
 LOCUS O991C09.s1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1455664 3'  
 DEFINITION similar to gb:M12529 APOLIPOPROTEIN B PRECURSOR (HUMAN);, mRNA  
 sequence.  
 ACCESSION AA863156  
 VERSION AA863156.1 GI:2955635  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 86)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-rc@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmer-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILM at:  
 www-bio.llnl.gov/bbrp/image/image.html  
 www-bio.llnl.gov/bbrp/image/image.html  
 Insert Length: 486 Std Error: 0.00  
 Seq primer: -40ml3 fwd. RT from Amersham.  
 Location/Qualifiers

```

source
1..86
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1455664"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Kids"
/notes="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AAGTCGAGAGATTGCGCGCGCATATTTTATTTTATTTT 3'] ,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT      13 a      28 c      21 g      24 t
ORIGIN

Query Match
Best Local Similarity 64.8%; Score 13.6; DB 9; Length 86;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 2 GATTCTAGCAATTCAAATC 21
11 GATTGTAGCCTTCAATC 30

RESULT 33
BZ762984/c 87 bp DNA linear GSS 13-MAR-2003
LOCUS
DEFINITION
Arabidopsis thaliana genomic clone SALK_110771.31.45.x, genomic
survey sequence.
BZ762984
BZ762984.1 GI:28935537
GSS
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 87)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadinab,
,C., Jeske,A., Karnes,M., Kim,C.U., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-indexed library of insertion mutations in the
Arabidopsis Genome
Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..87
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_110771.31.45.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can

```

```

BASE COUNT      35 a      17 c      10 g      25 t
ORIGIN
be found at http://signal.salk.edu/tdna_protocols.html"

Query Match
Best Local Similarity 64.8%; Score 13.6; DB 29; Length 87;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 AGATTCTAGCAATTCAAAT 20
68 AGCTTTTAGGTTTCAAT 49

RESULT 34
AL949242/c 90 bp DNA linear GSS 24-OCT-2002
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-319C03-015860,
genomic survey sequence.
AL949242
AL949242.1 GI:24405864
GSS
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FRS
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 90)
Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.
Direct Submission
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone F9H3. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1..90
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-319C03-015860"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector PAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT      32 a      11 c      15 g      30 t
ORIGIN
Query Match
Best Local Similarity 64.8%; Score 13.6; DB 29; Length 90;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

[illegible]

```

Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .92
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone_id="YK107d2"
/dev_stage="embryo"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2 hermaprodite embryo"
hermaprodite embryo"

BASE COUNT      22 a      20 c      19 g      31 t

Origins
Query Match          64.8%; Score 13.6; DB 14; Length 92;
Best Local Similarity 80.0%; Pred. No. 7.8e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2   GATTCTCAGGATTCGAATC 21
        |||||
Db       78 GAATTCAGGATTTAATTC 59

RESULT 37
LOCUS BH218165                      94 bp    DNA             linear     GSS 08-NOV-2001
DEFINITION 1006077E06.x1 1006 - Rescuemu Grid G Zea mays genomic, genomic survey sequence.
ACCESSION  BH218165
VERSION     BH218165.1 GI:16810606
KEYWORDS    GSS.

SOURCE      Zea mays
            Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 94)
            Walbot,V.

REFERENCE   Unpublished
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel.: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1006077 row: 27
            Class: transposon-tagged.

FEATURES
            Location/Qualifiers
                1..94
                    /organism="Zea mays"
                    /mol_type="genomic DNA"
                    /culivar="mixed background W23/A188/B73"
                    /db_xref="taxon:4577"
                    /tissue-type="leaf"
                    /dev_stage="adult"
                    /lab_host="DH10B"
                    /clone_lib="1006 - Rescuemu Grid G"
                    /note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmb.iastate.edu' and follow the links for 'Rescuemu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT      30 a      8 c      34 g      22 t

```

ORIGIN

Query Match 64.8%; Score 13.6; DB 28; Length 94;  
 Best Local Similarity 80.0%; Pred. No. 7.9e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTTCTAGGAATTC AAT 20  
 |||||  
 10 AGATTACGAGGAATTC AATT 29

RESULT 38  
 BM181183 96 bp mRNA linear EST 11-DEC-2001  
 LOCUS fw20c09.y1 Zebrafish C32 14 somite embryo Danio rerio cDNA clone  
 DEFINITION IMAGE:5565304 5', mRNA sequence.  
 ACCESSION BM181183.1 GI:17511546  
 VERSION BM181183.1  
 KEYWORDS EST.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 96)  
 Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shiu, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 Washu Zebrafish EST Project 1998  
 Unpublished

TITLE Washu Zebrafish EST Project 1998  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1..96  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /strain="C32"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:5565304"  
 /tissue\_type="embryo, 14 somite"  
 /lab\_host="DH10B"  
 /note="Vector: pAMP1. Site 1: EcoRI; Site 2: NotI; First strand cDNA synthesis was primed using oligo-dT on magnetic beads with an additional primer 5'-ggcgccgaatacgaactaccta-tagg-3'. Second strand synthesis was a 3-cycle PCR using the primers 5'-ggcgccgaatacgaactaccta-3', 5'-aagcagtgtaacaacgagagatctt-tttttttttv-3'. cDNA was subsequently amplified in a 7-cycle PCR with the following primers: 5'-ggcgccgaatacgaactaccta-3', 5'-aagcagtgtaacaacgagagatctt-tttttttttv-3', and a third PCR (5 cycles) and the primers 5'-caucacacacgagccgaatacgaactacctaagg-3' and 5'-caucacacacgagccgaatacgaactacctaagg-3'. Ends were treated with uracil DNA glycosylase and product with 3' overhangs was annealed to complementary ends of pAMP1. Insert can be excised using EcoRI and NotI. Library constructed by Joe Barnes and Steve Johnson (Washington

BASE COUNT 40 a 11 c 10 g 35 t  
 ORIGIN

Query Match 64.8%; Score 13.6; DB 12; Length 96;  
 Best Local Similarity 80.0%; Pred. No. 7.9e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 AGATTTCTAGGAATTC AAT 20  
 |||||  
 4 AGCTTCTATTAATTAAT AAT 23

RESULT 39  
 CNS000HH 96 bp DNA linear GSS 28-JUN-1999  
 LOCUS Arabidopsis thaliana genome survey sequence T7 end of BAC T6P22 of TACU library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.  
 DEFINITION Arabidopsis thaliana (thale cress)  
 ACCESSION AL090995.1 GI:5292135  
 VERSION AL090995.1  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana

REFERENCE  
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 96)  
 Samson, D., Saurin, W., Choise, N., Artiguenave, F., Brotier, P., Wincker, P., and Quetier, F.  
 Unpublished

JOURNAL 2 (bases 1 to 96)  
 REFERENCE  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefegenoscope.cns.fr - Web : www.genoscope.cns.fr)

FEATURES  
 source  
 1..96  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia"  
 /db\_xref="taxon:3702"  
 /clone="T6P22"  
 /clone\_lib="TAMU"  
 /note="end : T7"

BASE COUNT 32 a 21 c 22 g 21 t  
 ORIGIN

Query Match 64.8%; Score 13.6; DB 29; Length 96;  
 Best Local Similarity 80.0%; Pred. No. 7.9e+04;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GATTTCTAGGAATTC AATC 21  
 |||||  
 27 GAATCTTGGAATTC AATC 46

RESULT 40  
 BZ352958/c 100 bp DNA linear GSS 14-NOV-2002  
 LOCUS SALK\_119560.52.85.x Arabidopsis thaliana TUNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_119560.52.85.x, genomic survey sequence.  
 ACCESSION BZ352958  
 VERSION BZ352958.1 GI:24943820  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

REFERENCE  
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 100)

## AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

## JOURNAL

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g27020.  
Class: TDNA tagged.

## FEATURES

## source

Location/Qualifiers

1..100  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_119560.52.85.x"  
/note="11b="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## BASE COUNT

41 a 25 c 9 g 25 t

## ORIGIN

Query Match 64.8%; Score 13.6; DB 29; Length 100;  
Best Local Similarity 80.0%; Pred. No. 7.9e+04;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GATTCTAGAGATTCGAATC 21

Db 48 GATTTAGAGAGACTTGAATC 29

Search completed: February 4, 2004, 17:52:29  
Job time : 1250.23 secs